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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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June 29, 2004, 16:54:09; Search time 49.3653 Seconds (without alignments) 1562.545 Million cell updates/sec US-09-894-912A-13 1516 1 MGHLRLISWLPIILNFWEYI......QQKKRKVQDKQKSVSVSTVH 273 score: Title: Perfect Run on:

Scoring table: Sequence:

1586107 segs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000 Total number

Listing first 45 summaries Match 100% Post-processing: Minimum Match 0% Maximum

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2003as:*geneseqp2003bs:* A_Geneseq_29Jan04: geneseqp2001s:*geneseqp2002s:* geneseqp20048:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Human clo Human ste Secreted Human SCR SCR Human ste Human sec pol pol mat Human Мошве Mouse Description Aae13150 Abr62112 Abo44413 Abo44413 Aae13163 Aae13163 Aae13170 Aae13170 Aae13170 Aae13170 Aae13170 Abb61846 Abr62114 Abo44434 Aab93875 Abo44417 1 Aae13167 1 Abo44431 1 Abu52396 1 Abu52398 1 Abu52397 1 Abb11374 1 Aae13151 Aam78328 Aae13168 Aae13153 SUMMARIES ABO44427 AAW85607 AAB13170 ABR62114 ABO44434 AAB93875 AAE13168 AAE13150 AAE13153 AB044417 ABU52398 ABU52397 ABB11374 AB044114 AAB99220 ABR62112 AB044432 AAE13163 ABP61846 AAB13151 AAM78328 AAE13167 AB044431 8 Query Match Length 100.0 97.1 95.8 97.1 1505 1505 1505 1505 1505 1505 1472 1472 1452 1400 1400 1310.5 1310.5 1111 1472 1472 1472 Result ŝ

Aam79312 Human pro	Human	Abr62108 Secreted	Abr62115 Secreted				Abr62113 Mouse thr	Aae13162 Mouse thr	Abo44426 Mouse thr	Aae37115 Human sec	Abg76508 DNA encod	Abr62106 Secreted	Aae36166 Mouse SCR	Abr62101 Secreted	Abr62107 Secreted	Abr62102 Secreted	Adb76146 Novel hum	Aae13155 Human SCR	
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44405

ALIGNMENTS

Human; stem cell growth factor-like protein; antiinflammatory; nootropic; neuroprotective; vulnerary; cytostatic; anticonvulsant; immunostimulant; vasotropic; virucide; dermatological; tranquilliser; cerebroprotective; osteopathic; immunodeficiency syndrome; chronic granulomatous disease; duplicated immunodeficiency syndrome; wiskott-Aldrich syndrome; AIDS; acquired immunodeficiency syndrome; agammaglobulinaemia; thalassaemia; Gaucher's disease; lysosomal storage disease; mucopolysaccharidosis; parkinson's disease; Alzheimer's disease; thrombocytopaenia; SCID; severe combined immunodeficiency; immune disorder; autoimmune disease; parkinson's disease; alsorder; autoimmune disorder; autoimune pulmonary inflammation; cancer; tumour; gene therapy; SCR-1; supporting factor for the proliferation of stem cell. Human stem cell growth factor-like protein #3. AAE13151 standard; protein; 273 AA (first entry) 28-JAN-2002 AAE13151; RESULT 1 AAE1315 THE STATE OF THE S

40200177169-A2. Homo sapiena

05-APR-2000; 2000US-00543774. 28-JUN-2000; 2000US-0215733P. 09-JAN-2001; 2001US-00757562. 05-PBB-2001; 2001US-0266614P. 05-APR-2001; 2001WO-US011208 18-OCT-2001.

Drmanac RT; Liu C, Tillinghast JS, Sinku A, Liu (ckson M, Mize NK, Nishikawa M; Tang TY, Labat I, Tillingh Stache-Crain B, Dickson M,

(HYSB-) HYSBQ INC. (KIRI) KIRIN BEER KK.

WPI; 2001-657166/75. N-PSDB; AAD21725.

Human

Novel stem cell growth factor like polypeptides and polymucleotides for identifying modulators useful for treating diseases such as Alzheimer's

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The patent discloses novel stem cell growth factor-like proteins and polymucleotides encoding them. Proteins of the invention are also known as supporting factor for the proliferation of stem cells (SCR-1). Stem cell growth factor-like proteins are useful for supporting proliferation or cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell, embryonic stem cell, haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell cultured using stem cell growth factor-like proteins can replace as a graft for the bone marrow transplantation or cord blood transplantation for treating a variety of diseases such as immunodeficiency syndrome, agammaglobulinaemia, wiskott-Aldrich syndrome, agummaglobulinaemia, wiskott-Aldrich syndrome, agummaglobulinaemia, thalassaemia, haemolytic anaemia deto caryme defect, congenital anaemia such as sickle cell anaemia, Gaucher's disease, lysosomal storage diseases such as mucopolysactoharidosis, adrenal white matter diseases such as mucopolysactoharidosis, adrenal white matter care diseases and disorders such as Parkinson's disease, Alzheimer's disease and disorders such as severe combined immunodeficiency (SCID) and autoimmune pulmonary clubus sythematicus and disorders such as multiple sclerosis, systemic lupus sythematicus and disorders such as multiple sclerosis, systemic lupus sythematicus and disorders such as multiple sclerosis, systemic lupus sythematicus and disorders such as multiple sclerosis, systemic lupus sythematicus and disorders such as multiple sclerosis, systemic lupus sythematicus and the protein and autoimmune disorders such as multiple sclerosis, systemic lupus sythematicus and the protein and protein and protein and autoimmune disorders such as multiple sclerosis, systemic lupus sythematicus and the protein and pro
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cancer, rheumatoid arthritis, osteoporosis.
                                                                                                                                                                   Claim 28; Page 214-215; 232pp; English.
        disease,
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Sequence 273 AA;

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RLFFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFY 120
                                                                                                                                            LHLGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGPKRGTETRVREI 180
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Query Match 100.0%; Score 1516; DB 4; Length 273; Best Local Similarity 100.0%; Pred. No. 3.8e-111; Matches 273; Conservative 0; Mismatches 0; Indels 0.
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Stem cell growth factor-like protein; antianemic; anti-HIV; SCR-1; immunostimulant; vulnerary; haematopoietic stem cell; gene therapy; supporting factor for proliferation of stem cells; wound healing; haematopoietic progenitor cell; stromal cell; AIDS; thalassaemia; bone marrow transplantation; cord blood transplantation; chronic granulomatous disease; duplicated immunodeficiency syndrome; agammaglobulinaemia; Wiskott-Aldrich syndrome; haemolytic anaemla;
                                                                                                                                                                Human stem cell growth factor-like protein, SCR 1 #2.
                                       ABO44414 standard; protein; 273 AA
                                                                                                                        (first entry)
                                                                                                                      30-SEP-2003
                                                                              AB044414;
RESULT 2
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congenital anaemia; sicklaemia; Gaucher's disease; morphogenesis; epithelial cell growth; ovarian follicle development; nerve cell growth; cartilage remodeling; bone growth; immunosuppression; human.

Homo sapiens.

US2003044792-A1.

06-MAR-2003.

28-JUN-2001; 2001US-00894912.

28-JUN-2000; 2000US-0215733P. 05-FEB-2001; 2001US-0266614P. 05-APR-2001; 2001US-0282397P.

TANG Y T. LABAT I. TANG/)

LABA/

DRMANAC R T. MIZE N. NISHIKAWA M. (DRMA/) (MIZE/) (NISH/)

CHAO C. CHAO/) Chao C; Drmanac RT, Mize N, Nishikawa M, Fang YT, Labat I,

WPI; 2003-625403/59. N-PSDB; ACH04325

Novel isolated polypeptide having stem cell growth factor activity, useful for promoting wound healing, and as a medicine to proliferate or support human hematopoietic stem cells or human hematopoietic progenitor cells.

Claim 23; Page 72-73; 96pp; English.

The invention relates to an isolated stem cell growth factor-like collypeptide (referred as supporting factor for proliferation of stem cells (SCR-1)) from mouse or human, or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth carried carcivaty. Also included are an isolated polymucleotide encoding SCR-1 (or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity, or the complement of the polymucleotide), an (expression) vector comprising the SCR-1 polymucleotide, a host cell genetically engineered to contain the SCR-1 polymucleotide in operative association with a regulatory sequence of the SCR-1 polymucleotide in operative association with a regulatory sequence of the SCR-1 polymucleotide in the host cell, that controls expression of the SCR-1 polymucleotide in the host cell, that controls expression of the SCR-1 polymucleotide with stem cell growth factor activity and activity to support proliferation or survival of haematopoletic stem cell arching any 10 consecutive as from Aboyatala, an isolated SCR-1 polymeptide with stem cell growth factor activity and lacking any 10 consecutive as from Aboyatala, an isolated belymucleotide attached to a surface, a strond resident of the SCR-1 polymeptide or unique segment of the SCR-1 polymeptide to emportain conjugation or comprising the SCR-1 polymeptide or unique segment of the SCR-1 polymucleotide attached to a surface, a strond cell genetically engineered to express the SCR-1 polymeptide to support proliferation or survival of a stem cell and an implant comprising a cell or germ cell or germ cell and an implant comprising a cell or germ cell and the stem cell or strond or a stem cell or parm cell and the SCR-1 polymeptide as useful for identifying a compound that binds to support proliferation or a stem cell, a germ cell, a germ cell, or stem cell or the comprising survival of a stem cell or stem cell or derm cell or permentant number or service or po transplantation. The transplantation of haematopoietic stem cells can be employed as a therapy for treating diseases such as chronic granulomatous diseases, duplicated immunodeficiency syndrome, agammaglobulinaemia,

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27-APR-2000; 2000US-00560875.
20-JUN-2000; 2000US-00598075.
19-JUL-2000; 2000US-00650325.
01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-0065325.
20-CCT-2000; 2000US-00693325.
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                                                                                                                 Sequence 272 AA;
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Ma Y, Zhao QA,
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Wiskott-Aldrich syndrome, AIDS, etc., thalassaemia, haemolytic anaemia due to enzyme defect, congenital anaemia such as sicklaemia, Gaucher's disease etc. the SCR-1 polypeptide is useful for cell growth and morphogenesis, including tissue specific stem cell growth, epithelial morphogenesis, regulation, ovarian follicle development, promoting nerve cell growth, sustaining neuronal populations, cartilage remodeling, bone growth and immunosuppression. The present sequence is a Human SCR-1
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                                                                                                                                                                                                                                                                                                                               Human thrombospondin-30 and polynucleotide is useful in diagnosis and treatment of, e.g., malignant tumor, hemopathy, HIV infection, immunological diseases and various inflammatory diseases.
                                                                                                                                                                         1 MGHLRLISWLPIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGCCATCSDYNGCLSCKP
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                                                                                                                             Length 273;
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                                                                                                                            100.0%; Score 1516; DB 6; 100.0%; Pred. No. 3.8e-111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    malignant tumour; had
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N-PSDB; AAH45131.
                                                                                                                                        Local Similarity
                                                                                                      Sequence 273 AA;
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The present sequence is the protein sequence for human thrombospondin-30. Thrombospondin-30 protein and coding sequence are useful in the diagnosis and treatment of malignant theory, have semempathy, HIV infection, immunological diseases and various inflammation diseases. In addition
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, Chen R, Wang ZW;
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                                                                                                                                      thrombospondin-30 protein may be used for screening mimics, agonists, antagonists or inhibitors, or for use in peptide fingerprinting identification. The thrombospondin-30 coding sequence may be used as primers for nucleic acid amplification reaction or as probes for hybridisation reaction, or in producing gene chips or microarrays
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Wang D, Wang J, Zhang J, Ren F,
                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 99.3%; Score 1505; DB 4; L Local Similarity 100.0%; Pred. No. 2.8e-110; hes 271; Conservative 0; Mismatches 0;
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supporting factor for the proliferation of stem cell
                               Homo sapiens
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                                                                   Peptide
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                                                                                                                                   The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM89302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymerlectides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, infinibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; stem cell growth factor-like protein; antinflammatory; nootropic; neuroprotective; vulnerary; cytostatic; anticonvulsant; immunostimulant; vasotropic; virucide; dermatological; tranquilliser; cerebroprotective; osteopathic; immunodeficiency syndrome; fortonic granulomatous disease; duplicated immunodeficiency syndrome; Wiskott-Aldrich syndrome; AIDS; acquired immuno deficiency syndrome; agammaglobulinaemia; thalassaemia; Gaucher's disease; lysosomal storage disease; mucopolysaccharidosis;
                                                                     Nucleic acids encoding polypeptides with cytokine-like activities, useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adrenal white matter degeneration; anaemia; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; thrombocytopaenia; SCID; severe combined immunodeficiency; immune disorder; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune pulmonary inflammation; cancer; tumour; gene therapy; SCR-1;
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 Goodrich R;
                                                                                                            Claim 20; Page 3214-3215; 6221pp; English.
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Yang Y, Wejhrman T,
                                                                                  in diagnosis and gene therapy
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                            WPI; 2001-476283/51.
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                                         N-PSDB; AAX51461
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The patent discloses novel stem cell growth factor-like proteins and polymucleotides encoding them. Proteins of the invention are also known solymucleotides encoding them. Proteins of the invention are also known as supporting factor for the proliferation of stem cells (SKT-1). Stem cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell, embryonic stem cell, haematopoietic progenitor cell, historic cell, haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The proteins can replace as a graft for the bone marrow cell. action or cord blood transplantation for treating a variety of disease such as immunodeficiency syndrome, agammaglobulinaemia, wiskott-Aldrich syndrome, acquired immunodeficiency syndrome, agammaglobulinaemia, wiskott-Aldrich syndrome, acquired immunodeficiency syndrome (AIDS), wiskott-Aldrich syndrome, acquired immunodeficiency syndrome (AIDS), coch as sickle cell anaemia, Gaucher's disease, lysosomal storage deseneration, a variety of cancer and tumours. Proteins of the invention are useful for treating diseases such as severe combined immunodeficiency contenned and other neurodegenerative diseases, thrombocytopaenia, immune deficiencies and disorders such as severe combined immunodeficiency avere compined in manuely contenned and the contenned as severe combined immunodeficiency averemic.
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The present sequence is stem cell growth factor-like protein from human
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                                                                                                                                         22. .272 /note= "Human mature stem cell growth factor-like
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Stache-Crain B, Dickson M, Mize NK, Nishikawa M;
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                                                    1. .21
/label= Signal_peptide
ocation/Qualifiers
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09-JAN-2001; 2001US-00757562.
05-PEB-2001; 2001US-0266614P.
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Matches 271; Conservative
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(KIRI ) KIRIN BEBR KK
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Claim 28; Page 211-212; 232pp; English.
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LGKCLDNCPEGLEANNHTWECVSIVHCEVSEWNPWSPCTKKGKTCGPKRGTETRVREIIQ 182
                                               241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel stem cell growth factor like polypeptides and polynucleotides for identifying modulators useful for treating diseases such as Alzheimer's disease, cancer, rheumatoid arthritis, osteoporosis.
                                                                               HPSAKGNI.CPPTNBTRKCTVQRKKCQKGBRGKKGRBRKRKKPNKGBSKBAIPDSKSLESS
                                                                                           182 HPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKKGRERKRKKPNKGESKAIPDSKSLESS
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/note= "Human mature stem cell growth factor-like
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                                                                                                                                                                                                                                                                               Human stem cell growth factor-like protein #2
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/label=_Signal_peptide
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Stache-Crain B, Dickson M, Mize NK,
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2000US-0215733P.
2001US-00757562.
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(KIRI ) KIRIN BEER KK.
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The patent discloses novel stem cell growth factor-like proteins and polynucleotides encoding them. Proteins of the invention are also known as supporting factor for the proliferation of stem cells (SCR-1). Stem cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell or germ cell, pluripotent cell, paematopoietic stem cell, pluripotent cell, haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell cultured using stem cell growth factor-like proteins can replace as a graft for the bone marrow transplantation or cord blood transplantation for treating a variety of diseases such as immunodeficiency syndrome, chronic granulomations disease, duplicated immunodeficiency syndrome, chronic granulomation and sacket-Aldrich syndrome, acquired immune deficiency syndrome (AlbS), thalassaemia, haemolytic anaemia due to enzyme defect, congenital anaemia such as micopolysaccharidosis, adrenal white matter calculated cell for treating diseases such as mucopolysaccharidosis, adrenal white matter of the invention are useful for treating diseases such as severe comborytopaenia, immune deficiency congenic immune disease and other neurodegenerative diseases, thromborytopaenia, immune deficiency conservation are useful for treating diseases such as severe comborytopaenia, immune deficiency such as severe comborytopaenia, immune deficiency and disease and other neurodegenerative as severe comborytopaenia, immune
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Matches 271; Conservative
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Human stem cell growth factor-like protein, SCR 1 #4.

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The invention relates to new stem cell growth factor-like polypeptides and polynuclectides. The stem cell growth factor-like polypeptides and polynuclectides are useful for inducing differentiation of embryonic and adult stem cells to give rise to different cell types, for treating e.g. calesaes. They are also useful for generating new tissues and organs that can seful as hybridisation probes, oligomers or primers for PCR, for chromosome and gene mapping, in recombinantly producing protein, in candinantly producing protein, in candinantly producing protein, in candinantly producing protein, in companionantly companies and seaful for generating antibodies that specifically conditionant the polypeptide are useful for generating antibodies that specifically conditionant (e.g. protein or amino acid supplement, and as a carbon, nitrogen or carbohydrate source). Compositions comprising the current cor prevention of cancers, and other immunological disorders. The current sequence represents a human clone 1 throwbospondin protein
                                                                                                                                                                                                                                                                                                                                   New stem cell growth factor-like polypeptides and polynucleotides, use for treating e.g. leukemia, hemophilia and degenerative diseases like Alzheimer's disease, and for inducing immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Pig 1, 151pp, English
                                                30-AUG-2002; 2002WO-US027746.
                                                                                             2001US-0316368P.
                                                                                                                    10-DEC-2001; 2001US-0339739P.
19-APR-2002; 2002US-00125852.
                                                                                                                                                                                                                                                                                           WPI; 2003-381616/36.
                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 272 AA;
                                                                                             30-AUG-2001;
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63 PPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLH 122
                                                                                                                                                                               62 PFALERIGAKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLH 121
                                                                                                                                                                                                                                      123 LGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQ 182
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                                                                                                                                                                                                                                                                                                                     HPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGBSKBAIPDSKSLESS 242
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                                                                                                       2 HLRLISWLPIILNFWEYIGSQNASRGRRQRRWHPNVSQGCQGCCATCSDYNGCLSCKPRL
                                                                                                                                                                                                                                                                                                                                           182 HPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGBSKEAIPDSKSLESS
                                                                              HLRLISWLPIILNFWBYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRL
                                         GapB
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                                       0; Indels
99.3%; Score 1505; DB 6; L 100.0%; Pred. No. 2.8e-110; iive 0; Mismatches 0;
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                                       Matches 271; Conservative
                    Local Similarity
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ABO44432 standard; protein; 272 AA

30-SEP-2003 (first entry)

ABO44432;

ABO44432 ID ABO4 XX AC ABO4 XX DT 30-S

RESULT 8

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The invention relates to an isolated stem cell growth factor-like colypeptide (referred as supporting factor for proliferation of stem cells (SCR-1)) from mouse or human, or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity. Also included are an isolated polyuncleotide encoding C SCR-1 (or its mature protein portion, or fragment, analogue, variant or complement of the polyuncleotide), an (expression) vector comprising the complement of the polyuncleotide), an (expression) vector comprising the SCR-1 polyuncleotide in operative association with a regulatory sequence that controls expression of the polyuncleotide in the host cell, that controls expression of the SCR-1 polymeleotide which is an expression product of the SCR-1 polymeleotide (the polypeptide having an expression product of the SCR-1 polymeleotide (the polypeptide having an expression of comprise the as ascquence appearing as ABO44433), an isolated SCR-1 polymeleotide with stem cell growth factor activity and sequence does not comprise the as sequence appearing as ABO44433), an isolated polypeptide

Tacking any 10 consecutive ass from ABO44430, an isolated polypeptide

Tacking any 10 consecutive ass from ABO44430, an isolated polypeptide

The stam cell growth factor activity having at least an as sequence

The polymeleotide to maintain survival of or promote proliferation of a stem 22. .272 /notes "Mature stem cell growth factor-like protein. This protein is specifically claimed in claim 9" Novel isolated polypeptide having stem cell growth factor activity, useful for promoting wound healing, and as a medicine to proliferate or support human hematopoietic stem cells or human hematopoietic progenitor cells. Stem cell growth factor-like protein; antianemic; anti-HIV; SCR-1; immunostimulant; vulnerary; haematopoietic stem cell; gene therapy; supporting factor for proliferation of stem cells; wound healing; haematopoietic progenitor cell; stromal cell; AIDS; thalassaemia; bone marrow transplantation; cord blood transplantation; chronic granulomatous disease; duplicated immunodeficiency syndrome; agammaglobulinaemia; Wiskott-Aldrich syndrome; haemolytic anaemia; congenital anaemia; sicklaemia; Gaucher's disease; morphogenesis; epithelial cell growth; ovarian folliche development; nerve cell growth; cartilage remodeling; bone growth; immunosuppression; human. Chao C; Drmanac RT, Mize N, Nishikawa M, 1. .21 /label= Signal_peptide Location/Qualifiers Claim 23; Page 82; 96pp; English. 28-JUN-2000; 2000US-0215733P. 05-FRB-2001; 2001US-0266614P. 05-APR-2001; 2001US-0282397P. 28-JUN-2001; 2001US-00894912. DRMANAC R T. WPI; 2003-625403/59. MIZE N. NISHIKAWA M. Tang YT, Labat I, (TANG/) TANG Y T. (LABA/) LABAT I. N-PSDB; ACH04328 US2003044792-A1 CHINO C. Homo sapiens 06-MAR-2003 Peptide (LABA/) (DRMA/) (MIZB/) (NISH/) (CHAO/) Protein

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ccell or germ cell, an anti-SCR l antibody, a nucleic acid array

C comprising the SCR-1 polynucleotide or a unique segment of the SCR-1

C polynucleotide attached to a surface, a stronal cell genetically

c engineered to express the SCR-1 polypeptide to support proliferation or

Survival of a stem cell or germ cell and an implant comprising a cell

c genetically engineered to express the SCR-1 polypeptide to support

C proliferation or survival of a stem cell. The SCR-1

polypeptide is useful for identifying a compound that binds to the SCR-1

polypeptide and for maintaining survival of or promoting proliferation of

c a stem cell, a germ cell, a haematopoietic stem cell or a haematopoietic

c progenitor cell. The SCR-1 polypeptide is useful for promoting wound

CC progenitor cell culture using the SCR-1 polypeptide can replace as a

CR graft for the conventional bone marrow transplantation or cord blood

CR transplantation. The transplantation of haematopoietic stem cells can be

cransplantation. The transplantation of haematopoietic stem cells can be

cransployed as a therapy for treating diseases such as chronic granulomatous

diseases, duplicated immunodeficiency syndrome, agarmaglobulinaemia,

cransplantation syndrome, AIDS, etc., thalassaemia, haemolytic anaemia

due to enzyme defect. congenital anaemia such as sicklaemia, Gaucher's

disease etc. the SCR-1 polypeptide is useful for cell growth and

cell growth, and regulation, ovarian follicle development, promoting nerve

cell growth, and regulation, ovarian follicle development, promoting nerve

cell growth, and immunosuppression. The present sequence is a Human SCR-1
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Sequence 272 AA;

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                                                                                                        2 HLRLISWLFIILNFWEYIGSQNASRGRRQRRWHPNVSQGCQGGCATCSDYNGCLSCKPRL 61
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                                            Gaps
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Query Match 99.3%; Score 1505; DB 6; Length 272; Best Local Similarity 100.0%; Pred. No. 2.8e-110; Matches 271; Conservative 0; Mismatches 0; Indels (
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Stem cell growth factor-like protein; antianemic; anti-HIV; SCR-1; immunostimulant; vulnerary; haematopoietic stem cell; gene therapy; supporting factor for proliferation of stem cells; wound healing; haematopoietic progenitor cell; stromal cell; AIDS; thalassaemia; bone marrow transplantation; cord blood transplantation; chronic granulomatous disease; duplicated immunodeficiency syndrome; agammaglobulinaemia; Wiskott-Aldrich syndrome; haemolytic anaemia; congenital anaemia; sicklaemia; Gaucher's sidease; morphogenesis; epithelial cell growth; contained evelopment; nerve cell growth; cartilage remodeling; bone growth; immunosuppression; human.
                                                                                                                                                                                    Human stem cell growth factor-like protein, SCR 1 #1.
                                                ABO44413 standard; protein; 272 AA
                                                                                                                                         (first entry)
                                                                                                                                           30-SEP-2003
                                                                                             ABO44413;
RESULT 9
                          AB044413
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comprised (referred as supporting factor for proliferation of stem collypeptide (referred as supporting factor for proliferation of stem collypeptide (referred as supporting factor for proliferation of stem collypeptide (referred as supporting factor for proliferation or regament, analogue, variant or derivative, that retains stem cell growth factor activity, or the carry of the polymucleotide, an (expression) vector comprising the complement of the polymucleotide, an (expression) vector comprising the complement of the polymucleotide, an instance of the polymucleotide of the polymucleotide in operative association with a regulatory sequence that controls expression of the polymucleotide in peration of the polymucleotide in the host cell, preparation of the SCR-1 polymucleotide (the polymptide which is an expression product of the polymucleotide in the host cell, preparation of the SCR-1 polymucleotide with stem cell growth factor activity and activity to support poliferation or survival of haematopoidetic progenitor cell, with a provise that C-terminal as a sequence does not comprise the as sequence appearing as ABO444313, an isolated SCR-1 polymptide with stem cell growth factor activity and lacking any 10 consecutive ass from ABO44430, an isolated polypeptide with stem cell growth factor activity and call or gram cell, and an ABO44430, an isolated polypeptide to maintain survival of or promote proliferation of a stem cell or gram cell, an anti-SCR 1 antibody, a nucleic activity and cell or gram cell, an anti-SCR 1 antibody, a nucleic activity and cell or gram cell, an anti-SCR 1 polypeptide to support proliferation or survival of or promote proliferation or survival of a stem cell or gram 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated polypeptide having stem cell growth factor activity, useful for promoting wound healing, and as a medicine to proliferate or support human hematopoietic stem cells or human hematopoietic progenitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated stem cell growth factor-like
                                                                                                                                                                                                                                                                                                                                                                                         Chao
                                                                                                                                                                                                                                                                                                                                                                                         Fang YT, Labat I, Drmanac RT, Mize N, Nishikawa M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 23; Fig 3; 96pp; English.
                                                                                                                                                                      28-JUN-2000; 2000US-0215733P.
05-FEB-2001; 2001US-026614P.
05-APR-2001; 2001US-0282397P.
                                                                                                                                  28-JUN-2001; 2001US-00894912
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                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-625403/59.
                                                                                                                                                                                                                                                                                                                                NISHIKAWA M.
                                                      US2003044792-A1
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                    Homo sapiens.
                                                                                             06-MAR-2003.
                                                                                                                                                                                                                                                                                                          (MIZB/)
(NISH/)
(CHAO/)
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morphogenesis, including tissue specific stem cell growth, epithelial cell growth and regulation, ovarian follicle development, promoting nerve cell growth, sustaining neuronal populations, cartilage remodeling, bone growth and immunosuppression. The present sequence is a Human SCR-1 protein
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                                                                                                                                                                                                                                                                                                    PPALERIGMKOIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLH 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune pulmonary inflammation; cancer; tumour; gene therapy; SCR-1; supporting factor for the proliferation of stem cell; secreted protein.
                                                                                                                                                                                                                                                  HIRLISWLFIILNPMEYIGSQNASRGRRQRRHHPNVSQGCQGGCATCSDYNGCLSCKPRL
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                                                                                                                                                          Length 272;
                                                                                                                                                        99.3%; Score 1505; DB 6; Length 2' 100.0%; Pred. No. 2.8e-110; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein from clone DA228_6.
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28-JUN-2000; 2000US-0215733P.
09-JAN-2001; 2001US-00757562.
05-FRB-2001; 2001US-0266614P.
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Matches 271; Conservative
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(KIRI ) KIRIN BEER
                                                                                                                         Sequence 272 AA;
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The patent discloses novel stem cell growth factor-like proteins and polynucleotides encoding them. Proteins of the invention are also known as supporting factor for the proliferation of stem cells (SCR-1). Stem cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell, emrhance cell, germ cell, germ into stem cell, emrhance cell, paminodial or stem cell, paminodial or stem cell, paminodial or stem cell, paminodial or cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell cultured using stem cell growth catorilke proteins can replace as a graft for the bone marrow or transplantation or cord blood transplantation for treating a variety of diseases such as immunodeficiency syndrome, chronic granulomatous or disease, duplicated immunodeficiency syndrome, agammaglobulinaemia, wiskot-Aldrich syndrome, acquired immune deficiency syndrome (albeb), thalassaemia, haemolytic anaemia due to enzyme defect, congenital anaemia culs as sickle cell anaemia due to enzyme defect, congenital anaemia cliseases such as mucopolysaccharidosis, adrenal white matter degeneration, a variety of cancer and tumours. Proteins of the invention care useful for treating diseases such as Parkinson's disease, Alzheimer's deficiencies and disorders such as multiple sclerosis, alsease, Alzheimer's clisease and other neurodegenerative diseases, thrombocytopaenia, immune deficiencies and disorders such as multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, and autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, and autoimmune severe combined immune pulmonary inflammation. Sequence is human secreted protein from clone DA228_6
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                                                                                                                 polynucleotides for
such as Alzheimer's
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Sinku A, Liu C,
                                                                                                              Novel stem cell growth factor like polypeptides and identifying modulators useful for treating diseases disease, cancer, rheumatoid arthritis, osteoporosis.
Tang TY, Labat I, Tillinghast US, Sinku A, Liu Stache-Crain B, Dickson M, Mize NK, Nishikawa M;
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                                                                                                                                                                                                       Disclosure; Fig 3; 232pp; English
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Best Local Similarity 100.0
Matches 264; Conservative
                                                                   WPI; 2001-657166/75.
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immunostimulant; vulnerary; haematopoietic stem cell; gene therapy; supporting factor for proliferation of stem cells; wound healing; haematopoietic progenitor cell; stromal cell; AIDS; thalassaemia; bone marrow transplantation; cord blood transplantation; chronic granulomatous disease; duplicated immunodeficiency syndrome; agammaglobulinaemia; Miskott-Aldrich syndrome; haemolytic anaemia; congenital anaemia; sicklaemia; Guother's disease; morphogenesis; epithalial cell growth; ovarian follicle development; nerve cell growth; cartilage remodeling; bone growth; immunosuppression; human. growth factor-like protein; antianemic; anti-HIV; SCR-1;

Homo sapiens

US2003044792-A1

06-MAR-2003

28-JUN-2001; 2001US-00894912.

28-JUN-2000; 2000US-0215733P.

05-FBB-2001; 2001US-0266614P.

TANG Y T. LABAT I. (TANG/) (LABA/)

DRMANAC R T. MIZE N. NISHIKAWA M. (MIZE/) (NISH/) (DRMA/)

CHAO C.

CHAO/)

Chao C; Mize N, Nishikawa M, Drmanac RT, Labat I, rang YT,

WPI; 2003-625403/59.

Novel isolated polypeptide having stem cell growth factor activity, useful for promoting wound healing, and as a medicine to proliferate or support human hematopoietic stem cells or human hematopoietic progenitor cells.

Disclosure; Fig 3; 96pp; English.

The invention relates to an isolated stem cell growth factor-like polypeptide (referred as supporting factor for proliferation of stem collypeptide (referred as supporting factor for proliferation of stem cells (SCR-1)) from mouse or human, or its mature protein portion, or carlains stem cell growth factor activity. Also included are an isolated polymuclectide encoding SCR-1 (or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity, or the SCR-1 polymuclectide, a bolymuclectide, and polymuclectide in operative association with a regulatory sequence SCR-1 polymuclectide, a polympeptide which is an expression product of the SCR-1 polymuclectide in the host cell, preparation of the SCR-1 polymuclectide in the host cell, that controls expression product of the SCR-1 polymuclectide in the host cell, contain the scrivity to support proliferation or survival of hasmatopoietic stem cell captured for supposition with a provise that C-terminal as a cativity to support proliferation or survival of hasmatopoietic stem cell captured factor activity having at least an as sequence of sequence does not comprise the as sequence appearing as ABO44433, and contains and supposition of stem cell or grown factor activity having at least an as sequence comprising the SCR-1 polymuclectide or a unique sequence or polympetide to maintain survival of or promote proliferation or survival, of a stem cell and an isolated polypeptide to support proliferation or survival of a stem cell or germ cell and an implant comprising a cell comprise the scription or sequenced to express the SCR-1 polympetide to support proliferation or survival of a stem cell or germ cell and an implant comprising a cup or promoting proliferation or survival of a stem cell or germ cell or germ cell and an an expension of a stem cell, a germ cell, a paem cell, a hasmatopoietic stem cell or promoting proliferation or survival of a stem cell, a stem cell or germ cell or promoting proliferation or survival o

Treacy M;

Merberg D,

Mccoy JM, Lavallie ER, Racie LA,

Spaulding V, Agostino MJ;

Јасорв К,

WPI; 1999-024059/02.

(GEMY) GENETICS INST INC.

23-APR-1998;

ö healing. The human haematopoietic stem cell or human haematopoietic progenitor cell culture using the SCR-1 polypeptide can replace as a graft for the conventional bone marrow transplantation or cord blood transplantation. The transplantation of haematopoietic stem cells can be employed as a thorapy for treating diseases such as chronic granulomatous diseases, duplicated immunodeficiency syndrome, agammaglobulinaemia, wiskott-Aldrich syndrome, AIDS, etc., thalassaemia, haemolytic anaemia due to enzyme defect, congenital anaemia such as sicklaemia, Gaucher's disease etc. the SCR-1 polypeptide is useful for cell growth and morphogenesis, including tissue specific stem cell growth, epithelial cell growth, sustaining neuronal populations, cartilage remodeling, bone prowth and immunosuppression. The present sequence is a protein homologous to Human SCR-1 protein HPSAKGNICPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGESKEAIPDSKSLESS 242 241 62 FPALERIGHKOIGVCLSSCPSGYYGTRYPDINKCTXCKADCDTCFNKNFCTKCKSGFYLH 121 LGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQ 182 61 HLRLISWLF11LNFWEYIGSQNASRGRRQRRWHPNVSQGCQGGCATCSDYNGCLSCKPRL PPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCPNKNPCTKCKSGPYLH 0; Gaps Clone, secreted protein, protein factor; cytokine, lymphokine; interferon, colony stimulating factor; CSF; interleukin; cloning; tumour invasion; tumour suppression; immune boosting. Length 265; 97.1%; Score 1472; DB 6; Length 20 100.0%; Pred. No. 1.1e-107; ive 0; Mismatches 0; Indels 242 KEIPEQRENKQQQKGRKVQDKQKG 265 243 KEIPEQRENKQQQKKRKVQDKQKS 266 AAW85607 standard; protein; 292 AA Secreted protein clone da228_6. 98WO-US008336. 97US-00845296. 97.1%; 02-MAR-1999 (first entry) Matches 264; Conservative Similarity Sequence 265 AA; 24-APR-1998; Homo sapiens WO9849302-A1 25-APR-1997; 05-NOV-1998. AAW85607; m 63 123 183 Query Match Best Local S RESULT 12 **AAW**85607 8\$888888888888**\$**\$ ò g 8 셤 ઠે B ઠ 윰 Š

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The nucleotide sequence (NS) of the full-length protein-coding sequence of clones ci254 (AAV831312, da2286 (AAV83133), du4105 (AAV83134), eh801 (AAV83135), er3691 (AAV83136), fh1235 (AAV83137), fm601 (AAV83138) or fr4732 (AAV83139), (all clones are deposited as ATCC 98415) and the proteins they encode are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals for example, tumour suppression/invasion activity, immune system boosting activity. The polynucleotides are also believed to be useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; stem cell growth factor-like protein; antiinflammatory; nootropic; neuroprotective; vulnerary; cytostatic; anticonvulsant; immunostimulant; ostaotropic; viruotde; dermatological; tranquilliser; cerebroprotective; osteopathic; immunodeficiency syndrome; chronic granulomatous disease; duplicated immunodeficiency syndrome; ejammaglobulnaemia; thalassaemia; dauplicated immunodeficiency syndrome; syammaglobulnaemia; thalassaemia; daucher's disease; lysosomal storage disease; mucopolysaccharidosis; adrenal white matter degeneration; anaemia; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; thrombocytopaemia; SCID; servere combined immunodeficiency; immune disorder; antoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; autoimmune pulmonary inflammation; cancer; tumour; gene therapy; SCR-1; supporting factor for the proliferation of stem cell.
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                                          New polynucleotides encoding secreted human proteins - are derived from human foetal brain, adult brain, adult blood or placenta cDNA libraries, useful, e.g. as potential immunomodulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 HERLISWEPTILINFWEYIGSQNASRGRRQRRWHPNVSQGCQGGGATCSDYNGCLSCKPRL
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100.0%; Pred. No. 1.2e-107;
ive 0; Mismatches 0; Indels (
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                                                                                                                                     Claim 8; Page 63-64; 104pp; English.
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The patent discloses novel stem cell growth factor-like proteins and polymucleotides encoding them. Proteins of the invention are also known as supporting factor for the proliferation of stem cells (SCR-1). Stem cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell, or germ cell, germ line stem cell, embryonic stem cell, parabolatic stem cell, parabolatic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell cultured using stem cell growth cell. The haematopoietic progenitor cell cultured using stem cell growth cell. The haematopoietic progenitor cell cultured using stem cell growth catorine proteins can replace as a graft for the bone marrow crowt blood transplantation for treating a variety of disease such as immunodeficiency syndrome, chronic granulomatous wiskott-Aldrich syndrome, acquired immune deficiency syndrome (AIDS), thalassaemia, haemolytic anaemia due to enzyme defect, congenital anaemia such as mich cell anaemia due to enzyme defect, congenital anaemia desentation, a variety of cancer and tumours. Proteins of the invention care useful for treating diseases such as Parkinson's disease, Alzheimer's defenciencies and other neurodegenerative condenders condenders continued immune deficiency syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SCID)) and autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, and autoimmune pulmonary inflammation. Sequences of the invention are also useful in gene therapy. The present sequence is human SCR-1 related protein
                                                                                                                                                                                                                                                                                                                                                                         Novel stem cell growth factor like polypeptides and polynucleotides for identifying modulators useful for treating diseases such as Alzheimer's disease, cancer, rheumatoid arthritis, osteoporosis.
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ain B, Dickson M, Mize NK, Nishikawa M;
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                                                                          05-APR-2000; 2000US-00543774.
28-JUN-2000; 2000US-0215733P.
09-JAN-2001; 2001US-00757562.
05-FBB-2001; 2001US-0266614P.
                                       05-APR-2001; 2001WO-US011208
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(KIRI ) KIRIN BEER
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                                   Merberg
                              (EVAN/)
(MERB/)
                          JACO/)
                           (MCCO/)
                             (COLL/)
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WPI; 2003-381616/36 ABR62114; 63 rang YT; RESULT 1: 888888888888888 ð 셤 8 윤 셤 ð 셤 à ò The invention relates to human secreted or transmembrane protein (I), their fragments and is encoded by specific complementary decyribonucleic acid (cDNA) inserts (II), where the protein is substantially free from other mammalian proteins. (I) are useful for preventing, treating or prevention of tumours. (I) exhibits activity relating to angiogenesis, cytokine, cell proliferation, cell differentiation, antinflammatory, stem cell growth factor activity and activin or inhibin-related crytokine. (I) can be used to manipulate stem cells in culture to give crise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or cells damaged by illness, autoimmune disease, accidental damage or cells damaged by illness, between the proliferation of neural cells and central and peripheral nervous system diseases and neuropathies, such as a practimer's, Parkinson's disease, Huntington's disease, amycrophic central and peripheral nervous system diseases and neuropathies.

XI zheimer's, Parkinson's disease, Huntington's disease, amycrophic atteral sclerosis. (I) is involved in chemotactic or chemokinetic activity, regulation of haamatopolesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopaenia Human; cytostatic; antirheumatic; antiarthritic; vulnerary; analgesic; antiinflammatory; antibacterial; immunosuppressive; antiparkinsonian; neuropyrotective; nootropic; osteopathic; haemostatic; vasotropic; antiulocer; fungicide; antidibactic; antiasthmatic; antiallergic; immunostimulant; antiparasitic; secreted protein; transmembrane protein; cytokine; cell proliferation; cell differentiation; autoimmune disease; stem cell; growth factor; nervous system disease; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; osteoporosis; severe combined immunodeficiency; SCID; infection; multiple sclerosis; rheumatoid arthritis; gene therapy. Novel secreted or transmembrane protein and polynucleotide encoding the protein, useful for diagnosis and treatment of neurological disorders, cancer, autoimmune diseases, bone disorders and lung or liver fibrosis. Evans C; Collins-Racie LA, Claim 207; Page 203-204; 284pp; English 242 KEIPEQRENKQQQKKRKVQDKQKS 265 Lavallie ER, C ABP61846 standard; protein; 292 Human polypeptide SEQ ID NO 200 22-DEC-2000; 2000US-00745763. 98US-00040963 MCCOY J M. LAVALLIE E R. COLLINS-RACIE L A. 04-OCT-2002 (first entry) Treacy M, TREACY M. SPAULDING V. Mccoy JM, 2002-582343/62 EVANS C. MERBERG D. JACOBS K. N-PSDB; ABQ92060 US2002065394-A1 18-MAR-1998; Homo sapiens. ۵

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and for regeneration of bone, cartilage, tendon, ligament and/or nervetissue growth and in tissue repair, healing of burns, incisions, ulcers, for treating osteoprosis, osteoarthritis, bone degenerative disorders or periodontal disease. (1) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. (II) is useful to express recombinant protein, as markers for tissues in which the corresponding protein is preferentially expressed and in gene therapy. The present sequence is that of a polypeptide of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 HPSAKGNICPPTNETRKCTVQRKKCQKGRRGKKGRERKRKKPNKGRSKEAIPDSKSLESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 HIRLISWLPIILNFWEYIGSQNASRGRRQRRWHPNVSQGCQGCATCSDYNGCLSCKPRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 HIRLISWIFIIINPMEYIGSQNASRGRRORRMHPNVSQGCQGCATCSDYNGCLSCKPRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 LGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTXKGKTCGFKRGTETRVREIIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 HPSAKGNILCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGESKRAIPDSKSLESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.1%; Score 1472; DB 5; Length 2 100.0%; Pred. No. 1.2e-107; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR62114 standard; protein; 292 AA
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10-DBC-2001; 2001US-0339739P.
19-APR-2002; 2002US-00125852.
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Best Local Similarity 100.
Matches 264; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 292 AA;
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The wastern cell growth factor-like polypeptides and polymucleotides, useful for treating e.g. leukemia, hemophilia and degenerative diseases like Alzheimer's disease, and for inducing immune response.

XX XX

Disclosure; Fig 2; 151pp; English.

XX The invention relates to new stem cell growth factor-like polypeptides and polymucleotides. The stem cell growth factor-like polypeptides and polymucleotides are useful for inducing differentiation of embryonic and adult stem cells to give rise to different cell types, for treating e.g. CC dult stem cells to give rise to differentiation of embryonic and adult stem cells to give rise to differentiation of embryonic and adult stem cells to give rise to differentiation of embryonic and adult stem cells to give rise to differentiation of embryonic and in the Alzheimer's consecution and degenerating new tissues and organs that consecution and gene mapping, in recombinantly producing protein, in generating antisense DNA or RNA, in diagnostics as expressed sequence consequence and the polypeptides are useful for generating antibodies that specifically bind the polypeptides are useful for generating antibodies that specifically complypeptides are useful for generating antibodies that specifically contropen or carbohydrate source). Compositions comprising the corporation of cancers, and other immunological disorders. The current corporate source in complement, and as a carbon, corporation of cancers, and other immunological disorders. The current corporation of cancers, and other immunological disorders. The current corporations of polypeptides are useful clone da_288_6

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PPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLH 122 LGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQ 182 62 PFALERICARQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNRNFCTKCKSGFYLH 121 61 3 HLRLISWLFIILLNFWEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCXPRL 62 2 HLRLISWLFIILNFWEYIGSQNASRGRRQRRWHPNVSQGCQGGCATCSDYNGCLSCKFRL Gaps ő 97.1%; Score 1472; DB 6; Length 292; 100.0%; Pred. No. 1.2e-107; ive 0; Mismatches 0; Indels (KEIPEGRENKQQQKKRKVQDKQKS 266 Best Local Similarity 100. Matches 264; Conservative 123 122 63 Query Match 243 ઠ 셤 ઠે 셤 õ 셤 ð a ò

Search completed: June 29, 2004, 16:59:51 Job time : 66.6986 secs

242 KEIPEGRENKÓQÓKKRKVÓDKÓKS 265

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19 YIGSQNASRGRRQRRMHPNVSQGCQGGCATCSD--YNGCLSCKPRLFFALERIGMKQIGV
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1516
1 WGHLRLISWLFIILNFWEYI......QQXKRKVQDKQKSVSVSTVH 273
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  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-525-940-18
US-08-976-838-18
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US-09-214-555B-7
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US-09-214-555B-7
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| Sequence 2. Application US/08284941
| Patent NO. 5863756
| GENERAL INFORMATION:
| PAPPLICANT: BARR, PHILIP J
| APPLICANT: GENERAL COMPOSITIONS AND METHODS FOR PACE 4 AND TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS NUMBER OF SEQUENCES: 16
| CORRESPONDENCE ADDRESS: 16
| CORRESPONDENCE ADDRESS: 16
| CORRESPONDENCE ADDRESS: 16
| COUNTRY: USESSER: COLLEY GODWARD CASTRO HUDDLESON & TATUM STREET: FIVE PALO ALTO SQUARE CITY: PALO ALTO
| STREET: FIVE PALO ALTO SQUARE CONDUTER: BADDY disk COMPUTER: BADDY STREET: PROSE/MS-DOS / SOFTWARE: PALO ALTO NUMBER: 30092 |
| STATURNEY AGENT INFORMATION: A 435 |
| ATTORNEY AGENT INFORMATION: TELEPHONE: (415) 843-5070 |
| TELEPHONE: (415) 843-5070 |
| TELEPHONE: CHARACTERISTICS: |
| TELEPHONE: CHARACTERISTICS: |
| TENERA: GENERAL SACE |
| TENERA: GENERAL SACE |
| TELEPHONE: CHARACTERISTICS: |
| TENERA: GENERAL SACE |
| TENERA: GENERAL SACE |
| TELEPHONE: (415) 843-5070 |
| TELEPHONE: CHARACTERISTICS: |
| TENERA: GENERAL SACE |
| TENERAL 
                                    Sequence
Seq
US-09-640-173-186
US-09-713-550-186
US-09-713-550-186
US-09-113-825-2
US-08-185-432-17
US-08-185-432-17
US-09-132-769-3
US-07-862-021B-10
US-08-312-769-5
PCT-US93-03164-10
US-08-355-076-103
US-08-857-076-103
US-08-857-076-103
US-08-746-559A-5
US-08-746-559A-5
US-08-687C-2
US-08-687C-2
US-08-645-559A-5
US-08-645-559A-5
US-08-687C-2
US-08-687C-2
US-08-687C-2
US-08-687C-2
US-08-685-819-2
US-08-864-641B-18
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TYPE: amino acid
TOPOLOGY: linear
       807
807
1068
1068
1068
2555
807
807
807
807
807
816
1367
1367
   146.5
146.5
146.5
146
143.5
143.5
139
139
139
139
139
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Gaps

39;

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Query Match
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77 CLSSCPSGYYGTRYPDINKCTKCKADCDTCFNK-NPCTKCKSGFYLHLGKCLDNCPBGLB 135
                    19 YIGSONASRGRRORRMHPNVSQGCQGCATCSD--YNGCLSCKPRLFPALERIGMKQIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39;
                                                                                                                                                                                                   Sequence 2, Application US/08447642

Patent No. 5989890
GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J
APPLICANT: KIREPR, MICHABL C
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
TITLE OF INVENTION: PACE 4.1 GENE AND FOLYPEPTIDES IN CELLS
NUMBER OF SEQUENCES:
ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
STREET: FIVE PALO ALTO SQUARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.4%; Score 173.5; DB 2; Length 969; 28.8%; Pred. No. 1.2e-06; tive 16; Mismatches 54; Indels 39.
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.2e-06;
.es 54; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,642
FILING DATE: 23-MAY-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 ANNHIMBCVSIVHCEVSEWNPWSPCTKKGKTCG 168
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                                                                         136 ANNHIMECVSIVHCEVSEWNPWSPCTKKGKTCG 168
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APPLICATION NUMBER: US 08/284,941
APPLICATION NUMBER: US 08/284,941
APTORNEY/AGENT INPORMATION:
NAME: NELEY PH.D., RICHARD L.
REGISTRATION NUMBER: 30092
REFERENCE/DOCKET NUMBER: CHIR-009/01US
TELECOMMUNICATION INPORMATION:
TELEPAX: (415) 843-5070
TELEPAX: 380916 COOLEY PA
INPORMATION POR. SEQ ID NO: 2:
SEQUENCE CHARACTERIFICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 969 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
11.4
Best Local Similarity 28.8
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein US-08-447-642-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    838 PDSELIRCGECHH-
                                                                                                              838 PDSELIRCGECHH-
                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                            US-08-447-642-2
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RESULT 3 US-09-236-503-2

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GENERAL INFORMATION:
APPLICANT: Barr, Philip J
APPLICANT: Richer, Michael C
TITLE OF INVENTION: Compositions and Methods for PACE 4 and 4.1 Gene and
TITLE OF INVENTION: Compositions and Methods for PACE 4 and 4.1 Gene and
TITLE OF INVENTION: Polypeptides in Cells
FILE REFERENCE: CHIR-O09/0408
CURRENT APPLICATION NUMBER: US/09/236,503
CURRENT PILING DATE: 1999-01-25
EARLIER APPLICATION NUMBER: 08/447,642
EARLIER PILING DATE: 1995-05-23
EARLIER PILING DATE: 1994-08-02
EARLIER PILING DATE: 1992-03-09
WUMBER OF SEQ ID NOS: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.4%; Score 173.5; DB 3; Length 969; 28.8%; Pred. No. 1.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BARR, PHILIP J
APPLICANT: BARR, PHILIP J
APPLICANT: BARR, MICHABL
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: COOLEY GODWARD CASTRO HUDDLESON & TATUM
STREET: PIVE PALO ALTO
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02147A
FILING DATE: 19930309
CLASSIFICATION NUMBER: US 07/848,629
FILING APPLICATION NUMBER: US 07/848,629
FILING DATE: 09-MAR-1992
ATTORINEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 ANNHIMECVSIVHCEVSENNPWSPCTKKGKTCG 168
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REGISTRATION NUMBER: 30092
REFERENCE/DOCKET NUMBER: CHIR-009/00US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application PC/TUS9302147A GENERAL INFORMATION:
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC comparatible
OCMPUTER: PSYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
Sequence 2, Application US/09236503
Patent No. 6277590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 969
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ORGANISM: Homo sapiens
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Matches 44; Conserv
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TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 23:
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amino acid
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Matches 55; Conservative
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LENGTH: 799 amino acid
                       ; MOLECULE TYPE: protein US-08-525-940-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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      TOPOLOGY:
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US-08-976-838-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 YIGSQNASRGRRORRMHPNVSQGCQGGCATCSD--YNGCLSCKPRLFPALBRIGMKQIGV 76
                                                                                                                                                                                                                                                     11.4%; Score 173.5; DB 5; Length 969; 28.9%; Pred. No. 1.2e-06; tive 16; Mismatches 54; Indels 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Frankusoff, Alex
APPLICANT: Miranda, Duis R.
APPLICANT: Miranda, Duis R.
APPLICANT: Wolf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
TITLE OF INVENTION: ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                               54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 ANNHIMECVSIVHCEVSEWNPWSPCTKKGKTCG 168
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1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/368,852
FILING DATE: 01-JAN-1995
PRIOR APPLICATION NUMBER: US 08/088,322
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C1
FILECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2848-11-C1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23, Application US/08525940 Patent No. 5866351 GENERAL INFORMATION:
TELECOMMUNICATION INPORMATION:
TELEPHONE: (415) 494-7622
TELERA: (415) 657-0663
TELEX: 308016 COOLEY PA
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 969 amino acids
TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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Matches 44; Conservative
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STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
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                                                                                                                                                                                                              PCT-US93-02147A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 NHTME-----NPWSPCTKK 163
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                                                                                                                                                                                                                                                                      21 GSONASRGRRORRMHPNVSQGCQGGCATCSDYNG--CLSCKPRLFPALERIGMKQIGVCL
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Patent No. 5981259
GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 31
CORRESPONDENTS 31
CORRESPONDENTS Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
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Query Match 10.7%; Score 162; DB 2; Length 799; Best Local Similarity 22.3%; Pred. No. 9.4e-06; Matches 55; Conservative 33; Mismatches 81; Indels
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STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BEAPC COMPATIBLE
COMPUTER: BEAPC COMPATIBLE
COMPATING SYSTEM: PC-DOS/NS-DOS
SOCTWARE: PASTEMIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,838
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CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C2
TELECOMMINICATION INFORMATION:
TELEPHONE: (303) 863-9700
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138 NHTMB-----NPWSPCTKK 163
                                                                                                                                                                                                           747 GODCOPCHRPCATCAGAGADGCINCTEGYFMEDGRCVQSCSISYYPDHSSENGYKSCKKC 806
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21 GSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNG--CLSCKPRLPPALBRIGMKQIGVCL 78
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TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 10.7%; Score 162; DB 2; Length 881; Best Local Similarity 22.3%; Pred. No. 1e-05; Matches 55; Conservative 33; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,838
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION WHUBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C2
TELECOMMUNICATION INFORMATION:
TELEPHAN: (303) 863-0223
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21, Application US/08976838
Patent No. 5981259
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                         203 QRKKCQK 209
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                          138 NHTME-----NPWSPCTKK 163
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                                                                                                                                                                                                                                                                                    19 SSCPSG-YYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLHLGKCLDNCPEGLEAN 137
  21 GSQNASRGRRQRRMHPNVSQGCQGCATCSDYNG--CLSCKPRLFFALERIGMKQIGVCL 78
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Fatent No. 5866551
GENERAL INFORMATION:
FAPLICANT: Franzusoff, Alex
APPLICANT: Miranda, Luis R.
APPLICANT: Molf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES
TITLE OF INVENTION: ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.7%; Score 162; DB 2; Length 881; 22.3%; Pred. No. 1e-05; tive 33; Mismatches 81; Indels 7
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
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CLASSIFICATION: 514
PRICASIFICATION DATA:
APPLICATION NUMBER: US 08/368,852
FILING DATE: U1-JAN-1995
PRILING DATE: U1-JAN-1995
APPLICATION NUMBER: US 08/088,322
PRILING DATE: U7-JUL-1993
APPLICATION NUMBER: US 08/088,322
FILING DATE: U7-JUL-1993
APPLICATION NUMBER: US 08/088,122
REGISTRATION NUMBER: 32,020
REGISTRATION NUMBER: 2848-11-C1
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: amino acid
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Best Local Similarity 22.3'
Matches 55; Conservative
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MOLECULE TYPE: protein
US-08-525-940-21
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COUNTRY: U.S.A.
ZIP: 80203
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US-08-525-940-21
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Qy 138 NHTMSCVS 13. Db 1.1	SEQUENCE 18, Application US/08976838 Sequence 18, Application US/08976838 Sequence 18, Application US/08976838 Sequence 18, Application US/08976838 GENERAL INFORMATION: TITLE OF INVENTION: TITLE OF INVENTION: CORRESPONDENCE ADDRESS: ADDRESSES: ADDRESSES	Oy 79 SSCPSG-YYGTRYPDINKCTKCKADCDTCFNKTRCFTCKKSGFYLHJCAKCLDMCPEGLEAN 137 1 1 1 1 1 1 1 1 1
Qy 138 NHTME	-18 -18 -1866351 -18666351 -18 -18666351 -18 -18 -18 -18 -18 -18 -18 -18 -18 -1	Query Match 10,7%; Score 162; DB 2; Length 915; Best Local Similarity 22.3%; Pred. No. 1.18-05; Matches 55; Conservative 33; Mismatches 81; Indels 78; Gaps 12; Qy

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: 288 amino acids
amino acid
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US-08-368-852-15
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Patent No. 6380171
GENERAL INPORMATION:
PAPLICAMT: INPORMATION:
TITLE OF INVENITOT DE RECHERCHE CLINIQUE DE MONTRAL
TITLE OF INVENITOT DE RECHERCHE CLINIQUE DE MONTRAL
TITLE OF INVENITOT DE RO-PROTEIN CONVERTING ENZYME
TITLE OF INVENITON: PRO-PROTEIN CONVERTING ENZYME
CURRENT APPLICATION NUMBER: 19509/14,555B
CURRENT FILING DATE: 1999-01-04
PRIOR FILING DATE: 1990-01-04
PRIOR FILING DATE: 1997-04-25
PRIOR FILING DATE: 1997-04-25
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                  APPLICANT: INCENTION: PRO-PROTEIN CLINIQUE DE MONTRAL, TITLE OF INVENTION: PRO-PROTEIN CONVERTING ENZYME, FILE REFERENCE: PRO-PROTEIN CONVER ENZ. CURRENT APPLICATION NUMBER: US/09/214,555B CURRENT FILING DATE: 1999-01-04 PRIOR PILING DATE: 1999-01-04 PRIOR PLILING DATE: 1999-01-04 PRIOR PILING DATE: 1997-04-25 PRIOR PILING DATE: 1997-
                                                                                                                                                                                                                               Sequence 2, Application US/09214555B Patent No. 6380171 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 22.3%;
Matches 55; Conservative 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-5558-2
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; ORGANISM: Homo sapiens
US-09-214-5558-7
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QRKKCQK 209
                                                                   899 QRKVLQQ 905
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US-09-214-555B-2
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US-09-214-555B-7
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                                                                                                                                                                                                                                                      324 THCPDGSYQDTKK---NLCRKCSENCKTCTEPHNCTECRDGLSLQGSRCSVSCBDGRYFN 780
                                                                                                                                                                                                                                                                                                                                                         181 GQDCQPCHRPCATCAGAGADGCINCTEGYPMEDGRCVQSCSISYYFDHSSENGYKSCKKC 840
                                                                                                                                             138 NHTME-----NPWSPCTKK 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      841 DISCLTCNGPGFKNCTSCPSGYLLDLCMCOMGAICKDATBESWAEGGFCMLVKKNNLC-- 898
                                                                                                                                                                                                                 79 SSCPSG-YYGTRYPDINKCTKCKADCDTCFNKNPCTKCKSGFYLHLGKCLDNCPEGLEAN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                   164 GKTC-----GPKRGTB-----TRVRBIIQHPSAKGNLCPPTNETRKCTV 202
                                                                                                           21 GSONASRGRRORRMHPNVSQGCQGCATCSDYNG--CLSCKPRLFFALERIGMKQIGVCL
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                                                     78; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
APPLICANT: Franzusoff, Alex
APPLICANT: Miranda, Luis R.
TITLE OF INVENTION: CD4+ TLYMPHOCYTE PROTEASES
TITLE OF INVENTION: ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: CO
COUNTRY: U.S.A.
Query Match
10.7%; Score 162; DB 4; Length 915;
Best Local Similarity 22.3%; Pred. No. 1.1e-05;
Matches 55; Conservative 33; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

10.6%; Score 161; DB 1; Length 288;
Best Local Similarity 28.2%; Pred. No. 3.6e-06;
Matches 46; Conservative 25; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368,852
FILING DATE: 05-JAN-1995
CLASSIFICATION: 435
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NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REPERENCE/DOCKET NUMBER: 2848-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
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Patent No. 5691183
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247 B 247
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APPLICANT:
APPLICANT:
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APPLICANT
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                                     94 NKCTKCKADCDTCPNK--NPCTKCKSGPYLH--LGKCLDNCPEGLEANNHTMECVSIVHC 149
PECSEVGCDGPGPDHCND----CL----HYYYKLK----NNTRICVSSCPPGHY----HADK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NPPLICANT: Williams, P. Mickey
LPPLICANT: Wood, William, I.
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
                                                              150 EVSEWNPWSPCTKKGKTC-GPKRGTETRVREIIQHPSAKGNLC 191
                                                                                                                                                   113 -----RKCSENXKTCTEFHXCTECR-----DGLSLQGSRC 142
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CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
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PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/146,222
FILING DATE: 1999-07-28
APPLICATION NUMBER: PCT/US99/20594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
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APPLICATION NUMBER: PCT/US99/28564
FILING DATE: 1999-12-02
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FILING DATE: 1999-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US99/30095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US99/21090
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Grimaldi, Christopher J.
                                                                                                                                                                                                                                              Sequence 4, Application US/09907794A Patent No. 6635468 GENERAL INFORMATION:
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Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                   errara, Napoleone
ilvaroff, Ellen
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Gerritsen, Mary B
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Mather, Jennie P.
Pan, James
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                                                                                                                                                                                                                                                                                                     APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                Desnoyers, Luc
Baton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                        ong, Sherman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 CPGGCRNGGPCNERRICECPDGPHGPHCEKALCTPRCMNG-----GLCVTPGPCIC
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                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                 83;
                                                                                                                                                                                                                                                                                                                                10.5%; Score 158.5; DB 4; Length 379; 24.9%; Pred. No. 8.1e-06; tive 26; Mismatches 72; Indels 83
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2900-11-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 4
LENGTH: 379
LENGTH: 379
CREANISM: HOMO BAPIENB
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CURRENT APPLICATION NUMBER: US/09/905,125A
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Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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Gerritsen, Mary E
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Mather, Jennie P.
Pan, James
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Botstein, David
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Gao, Wei-Qiang
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Baton, Dan L.
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Best Local Similarity
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Query Match 10.5%; Score 158.5; DB 4; Length 379;
Best Local Similarity 24.9%; Pred. No. 8.1e-06;
Matches 60; Conservative 26; Mismatches 72; Indels 83; Gaps 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 -TWETRKCTVQRKKCOKGERGKKGRERKRK-----KPNKGESKEAIPDSKSLESSKEIP 246
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CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
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; ORGANISM: Homo sapiens
US-09-905-125A-4
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Sequence 13, Application US/09894912A

Sequence 13, Application Wold 1921
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH
TITLE OF INVENTION: FACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: FACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES
CURRENT PELING DATE: 2010-04-05
PRIOR PILING DATE: 2001-04-05
PRIOR PILING DATE: 2001-02-05-10
PRIOR PILING DATE: 2001-02-05-13
PRIOR PILING DATE: 2001-02-05-13
PRIOR PILING DATE: 2001-02-05-13
PRIOR PILING DATE: 2001-01-09
PRIOR PILING DATE: 2001-01-09
PRIOR PILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PATENTIN VERSION NUMBER: 09/543,774
NUMBER OF SEQ ID NOS: 48
                                  Sequence 18, Appl
Sequence 21, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 27, Appl
Sequence 13, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 9, Appl
Sequence 20, Appl
         US-09-894-912A-14

US-10-276-774-1744

US-10-125-852-18

US-10-125-852-24

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US-10-10-10-25-825-13

US-10-10-25-852-13

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US-10-125-852-13

US-10-125-852-15

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US-10-125-852-15

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ORGANISM: Homo sapiens
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APPLICANT: Tang et al.

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH

TITLE OF INVENTION: PATTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES

FILE REFERENCE: 28110/37260A

CURRENT APPLICATION NUMBER: US/09/894,912A

CURRENT FILING DATE: 2002-05-10

PRIOR PLING DATE: 2001-04-05

PRIOR PLING DATE: 2001-04-05

PRIOR PLING DATE: 2000-06-28

PRIOR PLING DATE: 2000-06-28

PRIOR PLING DATE: 2001-01-09

PRIOR APPLICATION NUMBER: 09/543,774

PRIOR PLING DATE: 2001-01-09

PRIOR APPLICATION NUMBER: 09/543,774

PRIOR PLING DATE: 2001-01-09

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PRIOR APPLICATION NUMBER: 09/543,774

PRIOR APPLICATION NUMBER: 2001-01-09

PRIOR APPLICATION NUMBER: 2001-01-01-09

PRIOR APPLICATION NUMBER: 2001-01-09

PRIOR APPLICATION 
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                                                                                                                                                   121 LHLGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREI 180
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                                                                                                                                                                                                                                                                                                                                                                                  241 SSKEIPBQRENKQQQKRRKVQDKQKSVSVSTVH 273
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: Sequence 10, Application US/09894912A

: Publication No. US20030044792Al

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-894-912A-10
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RESULT 3 US-09-894-912A-34 ; Sequence 34, Application US/09894912A

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US-10125-852-23

US-10125-852-23

Sequence 23, Application US/10125852

Sequence 23, Application No. US20030032034A1

SEQUENCE 23, Application No. US20030032034A1

GENERAL INFORMATION:

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH FACTOR-1

TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES

FILE REFREBUCE: HYS-43A

CURRENT PRILICATION NUMBER: US/10/125,852

CURRENT PILING DATE: 2002-08-20

FRIOR FILING DATE: 2001-08-30

FRIOR FILING DATE: 2001-08-30

FRIOR FILING DATE: 2001-03-05

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin version 3.1

SEQ ID NO 23

LENGTH: 272
                                                                               CELL GROWTH
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                                     GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Tang et al.

TITIE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL.

TITIE OF INVENTION: PACYOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES

FILE REPERENCE: 20110/372604

CURRENT APPLICATION NUMBER: US/09/894,912A

CURRENT APPLICATION NUMBER: US/08/894,912A

CURRENT APPLICATION NUMBER: To be assigned

PRIOR APPLICATION NUMBER: 60/266,614

PRIOR APPLICATION NUMBER: 60/266,614

PRIOR APPLICATION NUMBER: 60/215,733

PRIOR APPLICATION NUMBER: 09/57,562

PRIOR APPLICATION NUMBER: 09/57,562

PRIOR PILING DATE: 2001-09-05

PRIOR PILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PATENTIN VERSION 3.0

LENGRH: 272

LENGRH: 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.3%; Score 1505; DB 10; Length 272; 100.0%; Pred. No. 1.3e-114; ive 0; Mismatches 0; Indels 0;
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Publication No. US20030044792A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
US-10-125-852-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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HPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGESKEAIPDSKSLESS 242
182 HPSAKGNLCPPTNBTRKCTVQRKKCQKGBRGKKGRBRKRKKPNKGBSKBAIPDSKSLBSS 241
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                                                                                                                                                                                                                                                                                                                                                                                    Merberg, David
Treacy, Maurice
Spaulding, Vikk
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 292;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/09/745,763
FILING DATE: 18-Jun-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 97.1%; Score 1472; DB 9; L
Best Local Similarity 100.0%; Pred. No. 6.6e-112;
Matches 264; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 219
CORRESPONDENCE ADDRESS:
ADDRESSES: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 166:
US-09-745-763-166
                                               243 KBIPBORENKOOOKKRKVQDKOKS 266
                                                                                       242 KBIPBORENKOOOKKRKVODKOKS 265
                                                                                                                                                                                                                                                                                             McCoy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sprunger, Suzanne A. REGISTRATION NUMBER: 41,323 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                   Sequence 166, Application US/09745763
Patent No. US20020065394A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (617) 498-828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 166:
SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
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                                                                                                                                                                                   US-09-745-763-166
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APPLICANT: Tang et al.

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH

TITLE OF INVENTION: PACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: PACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES

FILE REFERENCE: 28110/372604

CURRENT FILING DATE: 2002-05-10

FRIOR APPLICATION NUMBER: 60/266,614

PRIOR APPLICATION NUMBER: 60/266,614

PRIOR PELING DATE: 2001-04-05

PRIOR PILING DATE: 2001-04-05

PRIOR PILING DATE: 2001-01-09

PRIOR PILING DATE: 2001-01-09

PRIOR PILING DATE: 2000-04-05

PRIOR PILING DATE: 2000-04-05

WINDER OF SEQ ID NOS: 48

SOFTWARE: PACENTIN VONS: 48

SOFTWARE: PACENTIN VONS: 48

LENGTH: 265
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                                                                                                                                                                                                                                                                                                  LGKCLDNCPEGLEANNHTWECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQ 182
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                                                                                                                                             2 HLRLISWLFIILINFWEYIGSQNASRGRRQRRWHPNVSQGCQGCATCSDYNGCLSCKPRL
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                                                                                                              3 HLRLISWLFIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRL
                                                                      Gaps
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                         Score 1505; DB 14; Length 272; Pred. No. 1.3e-114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 265;
                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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100.0%; Pred. No. 5.9e-112;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 KEIPEQRENKQQQKKRKVQDKQKSVSVSTVH 272
                                        100.0%; Pred. ...
rive 0; Mismatches
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; Sequence 26, Application US/09894912A
; Publication No. US20030044792A1
; GENERAL INFORMATION:
                         99.38;
                       Query Match
Best Local Similarity 100.(
Matches 271; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 264; Conservative
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CORGANISM: Homo sapiens
US-09-894-912A-26
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US-09-924-12A-16

1S-09-924-12A-16

1S-09-912A-16

Sequence 16, Application US/09894912A

Publication No. US20030044792A1

GENERAL INFORMATION:

APPLICANT: Tang et al.

TITLE OF INVENTION: RECTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: FACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: PACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES

CURRENT APPLICATION NUMBER: US/09/894,912A

CURRENT FILING DATE: 2001-04-05

PRIOR PILING DATE: 2001-04-05

PRIOR PLILING DATE: 2001-02-05

PRIOR PLILING DATE: 2001-06-26

PRIOR PLILING DATE: 2001-01-09

PRIOR PLILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 46

SOFTWARE: PALENTIN Version 3.0

SEQ ID NO 16

LENGTH: 251

TYPE: PATE THE CONTINUED DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 46

SEQ ID NO 16

LENGTH: 251

TYPE: PATE TYPE: PATE TANGER DATE CONTINUED DATE CONTINUED DATE CONTINUED DATE CONTINUED DATE: TYPE: PATE TYPE: PATE TYPE CONTINUED DATE 
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length 292;
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97.1%; Score 1472; DB 14;
Best Local Similarity 100.0%; Pred. No. 6.6e-112;
Matches 264; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 2001-08-30
PRIOR PELICATION NUMBER: US 09/799,451
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
SEQ ID NO 25
LENGTH: 292
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US-09-894-912A-16
                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
US-10-125-852-25
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Publication No. US20030032034A1
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH PACTOR-I
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: HYS-43A
CURRENT APPLICATION NUMBER: US/10/125,852
CURRENT FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: US 60/316,368
                                                                                                                                                                                                                                                         RESULT 7

US-09-894-912A-48

Sequence 48, Application US/09894912A

Publication No. US20030044792A1

GENERAL INFORMATION:

APPLICANT Tang et al.

TITLE OF INVENTION:

FILLE REPERENCE: 28110/37260A

CURRENT PILLOATION NUMBER: US/09/894,912A

CURRENT PILLING DATE: 2002-05-10

PRIOR PILLING DATE: 2001-04-05

PRIOR PILLING DATE: 2001-04-05

PRIOR PILLING DATE: 2001-04-05

PRIOR PILLING DATE: 2001-02-05

PRIOR PILLING DATE: 2001-02-05

PRIOR PILLING DATE: 2001-01-02

PRIOR PILLING DATE: 2001-01-02

PRIOR PILLING DATE: 2001-01-03

PRIOR PILLING DATE: 2001-01-03
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           182 HPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGESKEAIPDSKSLESS 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEI PEQRENKOOOKKRKVODKOKS 266
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                                                                                       243 KEIPEQRENKQQQKKRKVQDKQKS 266
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US-10-125-852-25
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 32, Application US/09894912A

Publication No. US20030044792A1

GENERAL INFORMATION:

APPLICANT: Tang et al.

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/894,912A

CURRENT APPLICATION NUMBER: To be assigned

PRIOR APPLICATION NUMBER: 60/266,614

PRIOR APPLICATION NUMBER: 60/266,614

PRIOR PILLING DATE: 2001-04-05

PRIOR PILLING DATE: 2001-02-05

PRIOR PILLING DATE: 2001-04-05

PRIOR PILLING DATE: 2001-04-05

PRIOR PILLING DATE: 2000-06-28

PRIOR PILLING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 48

SEQ ID NO 32

LEAGTH: 279
183 HPSA--KGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGESKE--AIPDSKS 238
                                                                                                            181 QRXKCQKGERGKKGRERKRKKVPNKGESKEAIPDSKSLESSKEIPBÖRENKQQQKRRVQD 240
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                                                                                      143 CVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQHPSAKGNLCPPTNETRKCTV
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                                                                                                                                                                                                                                                                263 KQKSVSVSTVH 273
                                                                                                                                                                                                                                                                                           241 KQKSVSVSTVH 251
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US-09-894-912A-32
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RESULT 11 US-10-185-770-4

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Sequence 4, Application US/10185770
Publication No. US2003002217A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE OF INVENTION: USES THEREOF
FILE REPERENCE: CLOO01247
CURRENT APPLICATION NUMBER: US/10/185,770
FILE REPERENT FILING DATE: 2002-07-01
PRIOR PILING DATE: 2001-07-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 PPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCPNRNFCTKCKSGFYLH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 PFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCPNKNFCTKCKSGFYLH 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 225;
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; Bequence 1782, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
    APPLICANT: Morris, David W.
    TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER.
    FILE SPERENCE: 229452000122
    CURRENT APPLICATION NUMBER: US/10/087,192
    CURRENT FILING DATE: 2002-03-01
    PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR PILLING DATE: 2000-12-22
    PRIOR PILLING DATE: 2001-03-02
; RIUNG PALLICATION NUMBER: US 09/798,586
    PRIOR PILLING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FARESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.1%; Score 1275; DB 14;
100.0%; Pred. No. 5.5e-96;
tive 0; Mismatches 0;
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SOCITIVARES: PastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 224; Conservative
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US-10-087-192-1782
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-10-087-192-1782
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APPLICANT: Zhong, Mei
IIILE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOL
                                                                                                                                                                                                                                          63 PPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCT-KC---KADCDTCFNKNPCTKCKSG 118
                                                                                                                                                                                                                                                            62 PFALERIGAKQIGVCLSSCPSGYYGTRYPDINKCTSKCPHBKADCDTCFNKNFCTKCKSG 121
                                                                                                                                                                                                                                                                                                    119 FYLHIGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVR 178
                                                                                                                                                                                                                                                                                                                       122 FYLHIGKCLDNCPEGLEANNHTWECVSSVHCEVSENNPWSPCTKKGKTCGFKRGTETRVR 181
                                                                                                                                                                                  62
                                                                                                                                                                                                    2 HIRLISWIPTIINPWEYIGSQNASRGRRQRRWHPNVSQGCQGCATCSDYNGCLSCRPRL 61
                                                                                                                                                                               3 HLRLISWLFIILNFWEYIGSQNASRGRRQRRWHPNVSQGCQGGCATCSDYNGCLSCKPRL
                                                                                                                                                  Gaps
                                                                                                                                                  4,
                                                                                                                      Length 239;
                                                                                                                                                  Indels
                                                                                                                    Score 1178; DB 15;
Pred. No. 4.6e-88;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                  179 BIIQHPSAKGNLCPPTNETRKCTVQRKKCQKGBRG 213
                                                                                                                                                                                                                                                                                                                                                                                       182 BIIQHPSAKGNLCPPTNETRKCTVQRKKCQKGERG 216
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CURRENT APPLICATION NUMBERS: US/10/094,886
CURRENT FILING DATE: 2002-03-07
PRIOR PELING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/313,182
PRIOR PLILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/288,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 176, Application US/10094886 Publication No. US20040002120A1 GENERAL INFORMATION:
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Taupier, Raymond J., Jr.
Miller, Charles
Casman, Stacie
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APPLICANT: Tchernev, Velizar T.
APPLICANT: Liu, Xiachong
APPLICANT: Spytek, Kimberly A.
APPLICANT: Patturajan, Meera
APPLICANT: Buturajan, Meera
APPLICANT: Bregess, Catherine
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Shimkets, Richard
Rastelli, Luca
Spaderna, Steven
LaRochelle, William
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Gorman, Linda
Malyankar, Uriel M.
Boldog, Ferenc
Guo, Xiaojia
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Gangolli, Bsha
Gusev, Vladimir
Smithson, Glennda
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Gerlach, Valerie
Pochart, Pascal
                                                                                                                      Query Match
Best Local Similarity 97.7
Matches 210; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shenoy, Suresh
NUMBER OF SEQ ID NOS: 298
SOFTWARE: Patentin 2.1
SEQ ID NO 172
LENGTH: 239
                                                            TYPE: PRT
ORGANISM: Homo sapiens
US-10-094-886-172
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                                                              LGKCLDNCPEGLEANNHTFMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQ 182
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                                                                                                                       HPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRK 222
                                                                                                                                         HPSAKGNLCPPTNETRKCTVQRKKCQKGERGTIIGEEKKK 239
                                                                                                                                                                                                                            Sequence 172, Application US/10094886
Publication No. US20040002120A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Tchernev, Velizar T.
APPLICANT: Liu, Xiaohong
APPLICANT: Datturajan, Meera
APPLICANT: Batturajan, Meera
APPLICANT: Burgess, Catherine
APPLICANT: Vernet, Corine A.
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Taupier, Raymond J., Jr.
Miller, Charles
Casman, Stacie
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Gangolli, Bsha
Gusev, Vladimir
Smithson, Glennda
Zerhusen, Bryan
Gerlach, Valerie
Pochart, Pascal
Pernandes, Blma
Shimkets, Richard
Rastelli, Luca
Spaderna, Steven
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Malyankar, Uriel M.
Boldog, Perenc
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Shenoy, Suresh
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US-10-094-886-172
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PRIOR FILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-08-21
PRIOR PILING DATE: 2001-08-21
PRIOR PILING DATE: 2001-03-09
PRIOR PILING DATE: 2001-08-07
PRIOR PILING DATE: 2001-08-07
PRIOR PILING DATE: 2001-08-21
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Publication No. US20040002120A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A.
APPLICANT: Patturajan, Meera
APPLICANT: Burgess, Catherine
APPLICANT: Vernet, Corine A.
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Boldog, Ferenc
Guo, Xiaojia
Shenoy, Suresh
Padigaru, Muralidhara
Taugher, Raymond J., Jr.
Miller, Charles
FILING DATE: 2001-05-02
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Zerhusen, Bryan
Gerlach, Valerie
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Gangolli, Esha
Gusev, Vladimir
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Gorman, Linda
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-094-886-176
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APPLICANT: LARCCHELLE, MILLIAM
APPLICANT: LARCCHELLE, WILLIAM
APPLICANT: LARCCHELLE, WILLIAM
APPLICANT: LARCCHELLE, WILLIAM
APPLICANT: Zhong, Mei
TITILE REPERENCE: 21402-290 B
CURRENT APPLICATION NUMBER: US/10/094,886
CURRENT APPLICATION NUMBER: 00/274,322
FRIOR APPLICATION NUMBER: 60/274,322
FRIOR APPLICATION NUMBER: 60/274,322
FRIOR APPLICATION NUMBER: 60/274,328
FRIOR APPLICATION NUMBER: 60/28,052
FRIOR PILLING DATE: 2001-09-10
FRIOR PILLING DATE: 2001-09-10
FRIOR APPLICATION NUMBER: 60/274,281
FRIOR APPLICATION NUMBER: 60/274,281
FRIOR APPLICATION NUMBER: 60/274,194
FRIOR APPLICATION NUMBER: 60/274,194
FRIOR APPLICATION NUMBER: 60/274,194
FRIOR PILLING DATE: 2001-03-08
FRIOR APPLICATION NUMBER: 60/274,194
FRIOR PILLING DATE: 2001-03-08
FRIOR FILING DATE: 2001-03-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GSQNASRGRRQRRWFIPWSQGCRGGCATCSDYNGCLSCKPRLFPALERIGMKQIGVCLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 298 SOFTWARE: Patentin 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.0%; Score 1107; DB 15; Length 195; 99.5%; Pred. No. 2.2e-82; tive 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: June 29, 2004, 17:15:57 Job time: 40.7755 secs
Fernandes, Elma
Shimkets, Richard
                                                                                             Rastelli, Luca
Spaderna, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 TVQRKKCQKGERG 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-10-094-886-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 174
```

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

June 29, 2004, 16:56:05; Search time 13.915 Seconds (without alignments) 1887.186 Million cell updates/sec

US-09-894-912A-13 Title: Perfect score:

1516 1 MGHLRLISWLFIILNFMEYI......QQKKRKVQDKQKSVSVSTVH 273 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	furin (BC 3.4.21.7	serine proteinase	subtilisin-like pr	subtilisin-like pr	furin (EC 3.4.21.7	subtilisin-like pr	probable proprotei	PACE4A - mouse (fr	subtilisin-like pr	subtilisin-like pr	subtilisin-like pr	hypothetical prote	Whit inhibitory fac	gene PACE4 protein	F-spondin precurso	protein bli-4D [im	Motch B protein -	insulin-like growt	Xotch protein - Af	cell-fate determin	probable kexin (BC	hypothetical prote	P-spondin - rat	Wnt inhibitory fac	trophozoite cystei	insulin-like growt	notch protein homo	protein-tyrosine k	notch protein homo
SUMMARIES	ΩI	T43251	534583	JC5571	JC5570	A43434	A39490	B48225	152527	A48225	G02428	JC6148	T24232	A59180	153282	A47723	D87803	A49175	A33837	A35844	A49128	T37314	T27283	A38152	B59180	C42125	IGHUR1	A40043	870713	S18188
	BB	~	7	7	~	7	-	7	~	-	N	7	~	~	N	N	~	~	N	~	~	~	~	7	~	~	-	~	N	7
	Length	1299	1548	962	975	1680	696	915	932	915	899	915	440	379	937	803	942	1203	1371	2524	2471	570	1620	807	378	677	1367	2555	1369	2531
مين	Query Match	12.7	12.3	12.1	12.1	11.6	11.4	11.1	11.0	11.0	10.7	10.7	10.6	10.5	10.3	10.3	10.1	9.9	9.8	9.8	9.7	9.6	9.6	9.5	9.4	9.4	9.5	9.5	9.1	9.1
	Score	192	186.5	184	184	176.5	173.5	168	167.5	167	162	162	161	158.5	156.5	156	153.5	150.5	149	148.5	147.5	145	145	143.5	142	142	139	139	138.5	138
	Result No.	-	7	m	4	ß	9	7	æ	60	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

notch-1 protein -	transmembrane prot	insulin receptor-r	insulin receptor p	hypothetical prote	insulin receptor p	insulin receptor p	insulin receptor (insulin receptor -	apoptosis-mediatin	insulin receptor-r	Notch homolog Moto	hypothetical prote	trophozoite surfac	furin (BC 3.4.21.7	cysteine rich prot
A46019	S42612	B47417	INHUR	T26972	A34157	A36080	S57245	A56081	A46484	B36502	A48825	T22812	A48579	843656	T42017
~	~	N	Н	N	N	~	N	н	~	~	N	~	N	~	N
331	437	540	1382	1111	1372	1383	2101	2148	327	1268	861	3871	667	837	1274
5	N														
9.1 25	9.0	0	6.8	8.9	8.9	6.8	8.5	8.5	8.4	8.4	8.4	8.3	8.3	8.5	8.2
138 9.1 29	137 9.0 2	0					129.5 8.5			128 8.4				125 8.2	

ALIGNMENTS

RESULT 1
T43251
furin (BC 3.4.21.75) - fall armyworm
N'Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serin
C.Species: Spodoptera frugiperda (fall armyworm)
C;Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text change 11-Jan-2000
C,Accession: T43251
R; Cieplik, M.; Klenk, H.
submitted to the EMBL Data Library, January 1996
A; Description: Cloning and functional characterization of FURIN from Spodoptera frugiper
A;Reference number: Z22368
A; Accession: T43251
A;Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-1299 < CIB>
A; Cross-references: EMBL: Z68888; NID: 91167859; PID: e219690; PIDN: CAA93116.1
A;Experimental source: clone Sfurin 6; ovary
C; Function:
A; Description: responsible for the endoproteolytic processing of proproteins with specif:
C; Keywords: hydrolase; serine proteinase
Query Match 12.7%; Score 192; DB 2; Length 1299;
Best Local Similarity 27.8%; Pred. No. 2.6e-05; Matches 63; Conservative 26; Mismatches 78; Indels 60; Gaps 12;

37 NVSQGCQGGCATCSD-YNGCLSCKPRLPPALERIGMKQIGVCLSSCPSGYYGTRYPDINK 95 윱

96 CTKCKADCDTCF--NKNFCTKCKSGFYLHLGKCLDNCPEGLBANNHTMECVSIVHCEVSB 153 154 WNPWSPCTKKGKTCGFKRGTBTRVREIIQHPSAKGNLCPP---TNETRKC-TVQRKKCQK 209 900 ---CSTCT-----SAFCLSCEPKWBLNKKGKCMPVGSDKCSA 933 g g ઠે Š

210 GERGKKGRERKRKKPNK-----GESKB---AIPDSKSLESSKEIPB 247

ò

d

RESULT 2 S34583

Gerine proteinase (BC 3.4.21.-) PC6B - mouse
GiSpecies: Mus musculus (house mouse)
GiSpecies: Mus musculus (house mouse)
GiAccession: S34583
R;Nakagawa, T.; Murakami, K.; Nakayama, K.
FRBS Lett. 377, 165-171, 1993
A;Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a }
A;Reference number: S34583; MUID:93327934; PMID:8335106

```
subtilisin-like proprotein convertase (EC 3.4.21.-) PACB4 precursor, splice form E-I - I C;Species: Homo sapiens (man)
C;Date: 1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C;Accession: JC5570
R;Mori, K.; Kii, S.; Tsuji, A.; Nagahama, M.; Imamaki, A.; Hayashi, K.; Akamatsu, T.; Ni Biochem. 121, 941-948, 1997
A;Title: A novel human PACB4 isoform, PACB4B is an active processing protease containing A;Reference number: JC5570; MUID:97335942; PMID:9192737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: DDBJ:D87993; NID:g2330548; PIDN:BAA21791.1; PID:g2330549
A,Experimental source: brain cerebellum
C;Comment: This enzyme is a processing protease and responsible for processing of varion tis retained intracellularly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: A43434
R;Roebroek, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, B.
B;Roebroek, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, B.
Biol. Chem. 267, 17208-17215, 1992
A;Title: Cloning and functional expression of Dfurin2, a subtilisin-like proprotein proc
A;Reference number: A43434; MUID:92381036; PMID:1512259
                                                                                                                                                               825 FDSELIRGGECHHTCGTCVGPGREECIHCAKNPHFHDW----KCVPACGEGFYPE---- 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         737 YPGDTAARRCRR-----CHKGCETCSSRAATQCLSCR-RGFY-----HHQEMNT 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 ANNHIMEC------VSIVHCEVS-EWNPWSPCTKKGKTCGFKRGTETRVRE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 CLSSCPSGYYGTRYPDINKCTKCKADCDTCPNK-NPCTKCKSGPYLHLGKCLDNCPEGLE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 ANNHIMEC------VSIVHCBVS-EWNPWSPCTKKGKTCGFKRGTETRVRE 179
767 CVTLCPAGFYADE--SQKNCLKCHPSCKKCVDEPEKCTVCKEGFSLARGSCIPDCEPGTY 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 YIGSQNASRGRRQRRMHPNVSQGCQGGCATCSD--YNGCLSCKPRLFFALBRIGMKQIGV 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          furin (BC 3.4.21.75) 2 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       876 --EMPGLPHKVCRRYGPPGGB-RQATVS----SKGVPG--GQSLSASSPGAGE 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 IIQHPSAKGNIC----PPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGE 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----PPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 12.1%; Score 184; DB 2; Length 975; Best Local Similarity 26.6%; Pred. No. 7.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: JC5570
A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62; Conservative
                                                                                                                                                                                                                                                             180 IIQHPSAKGNLC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-975 < MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics:
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: J3-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C; Accession. JC5571
R; Mori, K.; Kii, S.; Tsuji, A.; Nagahama, M.; Imamaki, A.; Hayashi, K.; Akamatsu, T.; Na J. Biochem. 121, 941-948, 1997
J. Biochem. 121, 941-948, 1997
A; Title: A novel human PACE4 isoform, PACE4E is an active processing protease containing A; Reference number: JC5570; MUID:97335942; PMID:9192737
A; Accession: JC5571
A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Comment: This enzyme is a processing protease and responsible for processing of variou it is retained intracellularly.
                                                                                    A,Molecule type: mRNA
A,Residues: 1-1548 <NAK>
A,Cross-references: GB:D17583; NID:g407344; PIDN:BAA04507.1; PID:d1005033; PID:g440374
C,Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 KCTKCKADCDTCFNKNPCTKCKS----GPYLHLGKCLDNCPBGLEANNHTME-CVSIVHC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               925 SCERCSBDCVSCSGADLCQQCLSQPDNTLLLHEGRCYHSCPRGFYAKDGVCEHCSS--PC 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              880 NOPCHSSCKTC---NGSLCASCPTGMYLWLQ-----ACVPSCPQG----TWPSVTSG 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              724 YFGDTAARRCRR-----HHQEMNT 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 CLSSCPSGYYGTRYPDINKCTKCKADCDTCFNK-NFCTKCKSGFYLHLGKCLDNCPEGLE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 YIGSONASRGRRORRMHPNVSQGCQGGCATCSD--YNGCLSCKPRLFFALBRIGMKQIGV 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-962 <MOR>
A;Cross-references: DDBJ:D87994; NID:q2330550; PIDN:BAA21792.1; PID:g2330551
A;Experimental source: brain cerebellum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 SQCCQGCCATCSDYNG--CLSCKPRLFFALERIGMKQIGVCLSSCPSGYYGTRYPDI--N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 ------CPPT--NRTRKCTVQRKKCQXGERGKKGRERKRKKPNKGESKEAIPDS
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A;Cross-references: GDB:131390; OMIM:167405
A;Cross-references: GDB:131390; OMIM:167405
A;Map position: 15q26-15q26
C;Superfamily: subtilisin-like proteinase PACB4; subtilisin homology
C;Keywords: glycoprotein; bydrolase; serine proteinase
C;Keywords: glycoprotein; bydrolase; serine proteinase
F;1-62/Domain: superide #status predicted <PRO>
F;196-434/Domain: subtilisin homology <SBT>
F;398-954/Domain: subtilisin homology <SBT>
F;398-954/Domain: hydrophobic cluster #status predicted <HCL>
F;308-954/Domain: hydrophobic cluster #status predicted
F;205,246,347,420/Active site: App, His, Abn, Ser #status predicted
F;259/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                         77;
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                                                                                                                                                                                                                                                                                                     Length 1548;
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                                                                                                                                                                                                                                                                                                     12.3%; Score 186.5; DB 2; Length 1
25.0%; Pred. No. 6.8e-05;
ive 31; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1092 KALHNGLCLDECPEGTYKBERNDE 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 KSLESS---KEIPE----QRENKQ 253
                                                                                                                                                                                                                                                                                                                                                                                              66; Conservative
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                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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Best Local Similarity
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A;Gene: GDB:PACE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150
             Accession:
                                                                                                                                                                                                                                                                                                                                                                                              Matches
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C;Accession: B48225
R;Lusson, J.; Vieau, D.; Hamelin, J.; Day, R.; Chretien, M.; Seidah, N.G.
Proc. Natl. Acad. Sci. U.S.A. 90, 6691-6695, 1993
A;Title: CDNA structure of the mouse and rat subtilisin/kexin-like PC5: a candidate prop
A;Reference number: A48225; MUID:93342056; PMID:8341687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similar but not identical substrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB:L14933
C; Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C; Superfamily: subtilisin-like proteinase pace4; subtilisin homology
C; Keywords: duplication; glycoprotein; hydrolase; integrin binding; serine proteinase
F; 1-34 Domain: signal sequence #status predicted <81G>
F; 15-915/Product: probable proproprotein convertase 5 #status predicted <PRO>
F; 16-195/Product: probable proprotein convertase 5 #status experimental <PRO>
F; 16-402/Domain: subtilisin homology <PRO>
F; 16-402/Domain: subtilisin homology <PRO>
F; 173,214,388/Active site: Asp, His, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 PDINKCTKCKADCDTCFNKNF--CTKCKSGFYLH--LGKCLDNCPEGLEANNHTMECVSI 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 VHCEVSEWNPWSPCTKKGKTC-GPKRGTETRVREIIQHPSAKGNLCPPTNETRKCTVQRK 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 YIGSQNASRGRRQRRMHPNVSQGCQGCATCSDYN--GCLSCKPRLFFALBRIGMKQIGV 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PACB4A - mouse (fragment)
C;Species: Mus musculus (bouse mouse)
C;Species: Mus musculus (bouse mouse)
C;Accession: 15227
R;Hosaka, M.; Murakami, K.; Nakayama, K.
Biomed. Res. 15, 333-390, 1994
A;Tills: PACB4A is a ubiquitous endoprotease that has similar but not idential A;Reference number: 152527
                                                                                                                                                                                              probable proprotein convertase (EC 3.4.21.-) 5 precursor - rat
N;Alternate names: PC5 precursor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 23-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          683 ADKKRCRKCAPNCESCFGSHADQCLSCKYGYFLNEETSSCVAQCPEGSYQDIKKNIC---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58; Gaps
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A;Residues: 1-912 <RES>
A;Cross-references: GB:D50060; NID:9769700; PIDN:BAA08777.1; PID:9769701
C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
F;172-410/Pomain: subtilisin homology <SET>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
11.1%; Score 168; DB 2; Length 915;
Best Local Similarity 26.3%; Pred. No. 0.00075;
Matches 49; Conservative 25; Mismatches 54; Indels
| | | |
|---TCG 853
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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          :: : | |
838 PDSBLIRCGECHH-
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A;Molecule type: mRNA
A;Residues: 1-915 <LUS>
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R;Kiefer, M.C.; Tucker, J.B.; Joh, R.; Landsberg, K.B.; Saltman, D.; Barr, P.J.
BNA Call Biol. 10, 757-769, 1991
A;Title: Identification of a second human subtilisin-like protease gene in the fes/fps
A;Reference number: A39490; MID:92075167; PMID:1741956
A;Accession: A39490
A;Residues: 1-969 < KIB>
A;Residues: 1-969 < KIB>
A;Cross-references: GB:M80482; NID:gl89531; PIDN:AAA59998.1; PID:gl89532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form A
N;Alternate names: kexin homolog
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1038 HIAVID-LAVCLQFCPDGYFENS----RNRTCVP-----CEPNCASCQDHPEYCTSCDHH 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1088 LVMHEHK-----CYSACPLDTYET---EDNKCAPCHSTCATCNGPTDQDCTTCRSSR 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 YLHLGKCLDNCPEGLEANNHTWECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRV-R 178
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A;Nolecule type: mRNA
A;Residues: 1-1680 cR02>
A;Residues: 1-1680 cR03>
A;Residues: 1-1680 cR03>
A;Cross-references: GB:M94375; NID:g157461; PID:g157462
A;Note: sequence extracted from NCBI backbone (NCBIN:111933, NCBIP:111934)
A;Genetics:
A;Gene: Flybase:Pur2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 HLRLISWLPIILNFMBYIGSONASRGRRORRMHPNVSQGCQGGCATCSDY-NGCLSCKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 YIGSQNASRGRRQRRMHPNVSQGCQGCCATCSD--YNGCLSCKPRLFFALRRIGMKQIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 11.6%; Score 176.5; DB 2; Length 1680; Best Local Similarity 28.0%; Pred. No. 0.00033; Matches 60; Conservative 24; Mismatches 77; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 969;
                                                                                                                                                                                                                                                       A,Cross-references: PlyBase:FBgn0004598
C;Superfamily: subtilisin homology
C;Keywords: hydrolase; serine proteinase; transmembrane protein
F;409-652/Pomanin: subtiliain homology <SBT>
F;418,457,638/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1178 ECLONWI-----LNKRDKCIVSGSEGCSES 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 BIIQHPSAKGNLCPPTNBTRKCTVQRKK-CQKGE 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.4%; Score 173.5; DB 1
28.8%; Pred. No. 0.00034;
tive 16; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 ANNHIMBCVSIVHCEVSEWNPWSPCTKKGKTCG 168
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Matches 44; Conservative
A; Accession: A43434
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A;Cross-references: GB:U56387; NID:g1498312; PIDN:AAC50643.1; PID:g1498313
C;Comment: This protein functions as a soluble enzyme within the secretory pathway. It
                                              convertase (EC 3.4.21.-) 5 precursor - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           663 GHYHADK-KRCRKCAPN-----CBSCPGSHGDQCMSCKYGYFL-----NBETNSCV 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 SSCPSG-YYGTRYPDINKCTKCKADCDTCFNKNPCTKCKSGPYLHLGKCLDNCPEGLEAN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    825 DISCLITCHGEGFRANCTSCPSGYLLDLGMCQMGAICKDATEESWAEGGFCMLVKKRANLC-- 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CVS-----IVHCEVSEW-----NPWSPCTKK 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 GKTC-----GPKRGTE-----TRVREIIQHPSAKGNLCPPTNETRKCTV 202
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                                                                                                                                                                                                                                                                                                   A;Residues: 1-899 <REU>
A;Cross-references: EMBL:U49114; NID:g1218057; PIDN:AAA91807.1; PID:g1218058
C;Genetics:
                                                    gubtilisin-like proprotein convertase (EC 3.4.21.-) 5 precursor - human (fra
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Mar-2000
C;Accession: G02428
R;Reudelhuber, T.L.
submitted to the EMBL Data Library, Pebruary 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subtilisin-like proprotein convertase (EC 3.4.21.-) homolog - human
N;Alternate names: PC6A protease
C;Species: Homo sapiens (man)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 GSQNASRGRRQRRWHPNVSQGCQGCATCSDYNG--CLSCKPRLFFALERIGMKQIGVCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Superfamily: subtilisin-like proteinase PACE4; subtilisin homology C; Esywords: hydrolase; serine proteinase P;148-386/Domain: subtilisin homology <SBT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.7%; Score 162; DB 2; Length 915; larity 22.3%; Pred. No. 0.0019; Conservative 33; Mismatches 81; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.7%; Score 162; DB 2; Length 899; 22.3%; Pred. No. 0.0018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81; Indels
                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.7%
Best Local Similarity 22.3%
Matches 55; Conservative
                                                                                                                                                                                                                        A, Reference number: H01242
A, Accession: G02428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 QRKKCQK 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     883 ORKVLOO 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 NHTME----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 55; Conserv
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A; Regidues: 1-915 <MIR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Mus musculue (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
R;Lusson, J.; Vieau, D.; Hamelin, J.; Day, R.; Chretien, M.; Seidah, N.G.
Proc. Natl. Acad. Sci. U.S.A. 90, 6691-6695, 1993
A;Title: CDNA structure of the mouse and rat subtilisin/kexin-like PC5: a candidate prop. A;Reference number: A48225; MUID:93342056; PMID:8341687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Rosidues: 1-915 <1US>
A;Rosidues: 1-915 <1US>
A;Rosidues: 1-915 <1US>
B;Rosidues: 1-915 <1US>
A;Rosidues: 1-915 <10S>
B;Nakagawa, T.; Hosaka, M.; Toxii, S.; Watanabe, T.; Murakami, K.; Nakayama, K.
J. Biochem. 113, 132-115, 1993
A;Title: Identification and functional expression of a new member of the mammalian Kex2-A;Roference number: JX0248; MUID:93224489; PMID:8468318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A. Cross-references: DDBJ:D12619; NID:g220565; PIDN:BAA02143.1; PID:g220566
A;Note: the authors translated the codon GGC for residue 915 as Ala
C;Superfamily: subtiliain-lisin-lise proteinase PACEH; subtilisin homology
C;Superfamily: subtiliain-lisin-lise proteinase PACEH; subtilisin homology
C;Superfamily: subtiliain-lisin-lise proteinse PACEH; subtilisin homology
C;Superfamily: groppotein; pycoprotein; pycoprotein; pycoprotein; proprotein; proprotein proprotein proprotein proprotein convertase PC5 #status experimental <MAT>
F;117-915/Product: proprotein convertase PC5 #status experimental <MAT>
F;164-402/Domain: subtilisin homology <BBT>
F;173,214,388/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSCPSGYYGTRYPDINK -- CTKCKADCDTCFNKNFCTKCKSGFYLHLGKCLDNCPEGLEA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137 NNHTMB-----NPWSPCTK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          780 NGHDCQPCHRFCATCSGAGADGCINCTEGYVMEBGRCVQSCSVSYYLDHSSEGGYKSCKR 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      840 CDNSCLTCNGPGFKNCSSCPSGYLLDLGTCQMGAICKDATEESWAEGGFCMLVKKNNLC- 898
-----CHKGCETCTGRSPAQCLSCR-RGFY-----HHQETNT 742
                                                          CLSSCPSGYYGTRYPDINKCTKCKADCDTCPNK-NFCTKCKSGFYLHLGKCLDNCPEGLE 135
                                                                                             --VSIVHCEVS----EWNPWSPCTKKGKTCGFKRGTETR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 GSQNASRGRRQRRMHPNVSQGCQGCATCSDYNG--CLSCKPRLFFALERIGMKQIGVCL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 KGKTC-----GPKR------GT----GT----ETRVRBIIQHPSAKGNLCPPTNETRKCT 201
                                                                                                                                                                                                                     801 PDSBLVKCGECHHTCRTCVGPSREBCIHCAKSFHPQDWKCVPACGE-----GP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subtilisin-like proprotein convertase (BC 3.4.21.-) PC5 precursor N;Alternate names: kexin homolog; serine proteinase PC6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 11.0%; Score 167; DB 1; Length 915; Best Local Similarity 23.4%; Pred. No. 0.00088; Matches 58; Conservative 29; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                  177 VREIIQHPSAKGNLCPPTNETRKCTVQRKKCQKGER 212
                                                                                                                                                                                                                                                                                                                                      -----YPEEMPGL--PHKVCRRCBENCLSCEGSSR 876
     100 YFGDAAARRCRR-
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A; Residues: 1-915 <NAK>
                                                                                                                                                                      136 ANNHTMEC
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DD 679 GHYHADK-KRCRKCARNCESCPGSHGDQCMSCKYGYPLNBETNSCV 723	A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
OY 79 SSCPSG-YYGTRYPDINKCTKCKADCDTCPNKNPCTKCKSGPYLHLGKCLDNCPEGLEAN 137	A;Residues: 1-379 <bsi> A;Cross-references: GB:AF122922; NID:g4585369; PIDN:AAD25402.1; PID:g4585370</bsi>
724 THCPDGSYQDTTKMCRKCSENCKTCTBFHNCTEC	atch 10.5%; Score 158.5; DB 2; Length 379; cal Similarity 24.9%; Pred. No. 0.0016;
Qy 138 NHTMBCVSIVHCEVSEWNPWSPCTKK 163 : : : :	Matches 60; Conservative 26; Mismatches 72; Indels 83; Gaps 16; Qy 42 CQGCATCSDYNGCLSCKPRLFFALERIGMKQIGVCLSSC 81
Qy 164 GKTCGPKRGTBTRVRBIIQHPSAKGNLCPPTNBTRKCTV 202	bb 182 CPGGCRNGGFCNERRICECPDGFHGPHCBKALCTPROMGGLCVTPGFCIC 232
DD 841 DISCLTCNGPGFKNCTSCPSGYLLDLGMCQMGAICKDATEESWAEGGFCMLVKKNNLC 898	OY 82 PSGYYGTRYPDINKCTKC-KADCD-TCFNRNFCTKCKSGFYLHLGKCLDNCPBGLRANNH 139
QY 203 QRKKCQK 209	rgvncbrg
Db 899 QRKVLQQ 905	Qy 140 TMBCVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVRBIIQHPSAKGNLCPP 193
RESULT 12 T24232	194 - TNETRKCTVORKKCOKGRGKKGRRRKBKKPNKGBSKGAIPDSKSLESSKBIP
hypothetical protein R17.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans	319
C; Date: 15-UCT-1999 #sequence_revision 15-UCT-1999 #text_change 21-Jan-2000 C; Accession: T24232	Qy 247 B 247
Riballow, A. submitted to the EMBL Data Library, March 1997 A.Reference number: Z19860	Db 374 B 374
A;Accession: T24232 A;Status: preliminary; translated from GB/EMBL/DDBJ	RESULT 14
A, Molecule type: DNA A, Residues: 1-440 < WIL>	I55282 gene PACB4 protein - rat
A;Cross-references: EMBL:Z92809; PIDN:CAB07269.1; GSPDB:GN00021; CBSP:R17.3 A;Experimental source: clone R17	C;Species: Rattus norvegicus (Norway rat) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 22-Jun-1999
C; Venetios: A; dene : CESP: R17.3 A; Man modition: 1	C;Accession: 153262 R;Johnson, R.C.; Darlington, D.N.; Hand, T.A.; Bloomquist, B.T.; Mains, R.E. Rndocrinology 135, 1178-1185, 1994
Aintrons: 36/3; 89/3; 179/2; 241/1; 306/1; 346/2 C;Superfamily: Caenorhabditis elegans hypothetical protein R17.3	A,Title: PACE4: a subtilisin-like endoprotease prevalent in the anterior pituitary and r A,Reference number: 153282; MUID:94349873; PMID:8070361
Query Match Best Local Similarity 23.7%; Pred. No. 0.0013;	A;Accession: 153282 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA
; Conservative 30	A,Residues: 1-937 <res> A,Cross-references: GB:L31894; NID:g496221; PIDN:AAA61987.1; PID:g496222</res>
QY S9 KPRLFPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSG 118	C;Genetics: A;Gene: PACB4 C;Superfamily: subtilisin-like proteinase PACB4; subtilisin homology
ON 119 FYLHLGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVR 178	F;177-415/Domain: gubtiligin homology <sbt></sbt>
226	Query Match 10.3%; Score 156.5; DB 2; Length 937; Best Local Similarity 23.6%; Pred. No. 0.0043; Matches 51; Conservative 24; Mismatches 80; Indels 61; Gaps 11;
OY 179 BIIQHPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGBSKBAIPDSKS 238	19 YIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDVNGCLSCKPRLFFALERIGN
2/2 NVIQHABKGGAACEFUKETCFVBCK	REPTO
OY 239 LESSKRIPBORRNKOOKKKKVODKOKSVSVSTVH 273 :: : :	Qy 77 CLSSCPSGYYGTRYPDINKCTKCKADCDTCPNK-NPCTKCKSGPYLHLGKCLDNCPRGLB 135 1 1 1 1 1 1 1 1 1
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C.Accession: A59180 R.Hsieh, J.C.; Kodjabachian, L.; Rebbert, M.L.; Rattner, A.; Smallwood, P.M.; Samos, C.E.	
Nature 398, 431-436, 1999 Nature 398, Aprille Aprotein that binds to Wht proteins and inhibits their activities A; Reference number: A59180; MUID:99215557; PMID:10201374 A; Accession: A59180	RESULT 15 A47723

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F-spondin precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 27-3uu-1994 #sequence_revision 27-3un-1994 #text_change 17-Nov-2000
C;Accession: A47723
R;Ruiz i Altaba, A.; Cox, C.; Jessell, T.M.; Klar, A.
Froc. Natl. Acad. Sci. U.S.A. 90, 8266-8272, 1993
A;Title: Ectopic neural expression of a floor plate marker in frog embryos injected with A;Reference number: A47723
A;Accession: A47723
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A;Accession: A47723
A;Coss-references: GB:L09123; NID:g409244; PIDN:AAA19105.1; PID:g409245
C;Superfamily: Fspondin; thrombospondin type 1 repeat homology
F;435-489/Domain: thrombospondin type 1 repeat homology <THR1>
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Proprotein convertase subtilishin/kexin type 5 precursor (BC 3.4.21.-)
(Proprotein convertase PC5) (Subtilishin/kexin-like protease PC5) (PC6)
(Subtilisin-like proprotein convertase 6) (SPC6).
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SRQUENCE OF 330-1877 FROM N.A. (ISOFORM PCSB).
SRQUENCE OF TISSUE-Intestine;
MEDLINE=93327934; PubMed=8335106;
Nakagawa T., Murakami K., Nakayama K.;
Nakagawa T., Murakami K., Nakayama K.;
Nakagawa T. Murakami K., Nakayama K., Nakayama
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Constam D.B., Calfon M., Robertson B.J.;
"SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone
morphogenetic proteins at distinct sites during embryogenesis.";
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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TESSUB-Advenal cortex;

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LUSBON J., Vieau D., Hamelin J., Day R., Chretien M., Seidah N.G.;

LUSBON J., Vieau D., Hamelin J., Day R., Chretien M., Seidah N.G.;

CORA structure of the mouse and rat subtilisin/Kexin-like PC5: a

candidate proprotein convertase expressed in endocrine and
nonendocrine calls.;
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"Identification and functional expression of a new member of the mammalian Kex2-like processing endoprotease family: its striking structural similarity to PACE4.";
J. Blochem. 113:132-135(1993).
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TSSURE-BRAIN, and Intestine;
MEDLINE-93224409; PLUMGE-8468118;
Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.
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J. Cell Biol. 135:1261-1275(1996)
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InterPro; IPR000209; Peptidase_S8.

InterPro; IPR002284; Peptidase_S8B.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   **Rancourt S.L., Rancourt D.E.;

"Murine subtilisin-like proteinase SPC6 is expressed during embryonic implantation, somitogenesis, and skeletal formation.";

Dev. Genet. 21,75-81(1997).

-!- FUNCTION: Likely to represent a widespread endoprotease activity within the constitutive and regulated secretory pathway. Capable of cleavage at the RX(K/R)R consensus motif. May be responsible for the maturation of gastrointestinal peptides. May be involved in the cellular proliferation of adrenal cortex via the activation of growth factors.

-!- CATALYTIC ACTIVITY: Release of mature proteins from their proproteins by cleavage of Arg-Xaa-Yaa-ARG-|-Zaa bonds, where Xaa can be any amino acid and Yaa is Arg or Lys.

-!- SUBCELLULAR LOCATION: PC5A IS SECRETED THROUGH THE REGULATED SECRETORY PATHWAY. PC5B IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN: AC 1 and AC 2 (clusters of acidic amino acids) contain sorting information. AC 1 directs TGN localization and interacts with the TGN sorting protein PACS-1.
SIMILARITY: Belongs to peptidase family S8.
SIMILARITY: Contains 1 homo B/P domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bvent=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:97515; Pcsk5.
InterPro; IPR006212; Purin repeat.
InterPro; IPR009030; Grow_fac_recep.
                                                                                        MEDLINE=97436919; PubMed=9291583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D17583; BAA04507.1; -.
EMBL; D12619; BAA02143.1; -.
EMBL; L14932; AAA74636.1; -.
PIR; A48225; AAA225.
PIR; S34583; S34583.
HSSP; Q99405; IMPT.
MEROPS; S08.076; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTERNATIVE PRODUCTS:
                                                                   DEVELOPMENTAL EXPRESSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLY ENDOSOMES
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).

SIMILARITY) SIMILARITY) SIMILARITY)

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(POTENTIAL)

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1209 NOPCHSSCKTC---NGSLCASCPTGMYLWLQ-----ACVPSCPQG----TWPSVTSG 1253
                                                                                                                                                                                                                                                                                                                                                                                                39 SQGCQGCATCSDYNG--CLSCKPRLPPALERIGMKQIGVCLSSCPSGYYGTRYPDI--N 94
                                                                                                                                                                                          ٨
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 KCTKCKADCDTCFNKNPCTKCKS----GFYLHLGKCLDNCPEGLBANNHTMB-CVSIVHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 BVSEWNPWSPCTKKG-----KTC-----GFKRGTETRVRBIIQHPSAKGNL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----CPPT--NBTRKCTVQRKKCQKGBRGKKGRERKRKKPNKGBSKEAIPDS
                                                                                                                                                                                       GBYIDDOGHCOTCRASCAKCWGPTQEDCISCPVTRVLD
                                                                                                                                                                                                         ATEESWAEGGFCMLVKKNNLCQRKVLQQLCCKTCTPQG
                                                (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                             77;
                                                                                                                                                                                                                                                                                                                           ch 12.3%; Score 186.5; DB 1; Length 1877; 1 Similarity 25.0%; Pred. No. 6.5e-06; 66; Conservative 31; Mismatches 90; Indels 77;
                                                                                                                                      (POTENTIAL)
                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                               EC850E2DF20BA1C3 CRC64;
                                                                                                                                                                                                                                                       Missing (In isoform PC5A). /Frid=VSP_005439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1372 DPFLYNDMCHRSCPKSFYPDMRQCVPCHKNC----
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(GLCNAC.
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                                                    N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
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RESULT
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                                                                                                                                                                                                            PCK5_BRACL STANDARD; PRT; 1696 AA.
Q9NJI5; Q9NJ14; Q9NJ16;
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
                                                                                                                                                                                                                                                                                                                                                                                                                           ISOId=Q9NJ15-1; Sequence=VSP 005442, VSP 005443; DOMAIN: The propeptide domain acts as an intramolecular chaperone assisting the folding of the zymogen within the endoplasmic
                                                                                                                                                Branchiostoma californiensis (California lancelet) (Amphioxus).
Bukaryota, Metazoa, Chordata, Cephalochordata, Branchiostomidae,
                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=09NJ15-2; Sequence=VSP_005444, VSP_005445;
                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to peptidase family S8. SIMILARITY: Contains 1 homo B/P domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MESOFOS, SONO, ILL.

MESOFOS, SONO, URB; ...

INTERPRO; IPRO06212; Purin repeat.

INTERPO; IPRO06203; Grow fac_recep.

INTERPO; IPRO02003; Peptidase SB.

INTERPO; IPRO09203; Peptidase SB.

INTERPO; IPRO09203; Portease Inhib.

Pfam; PRO0483; P. Proprotein; I.

Pfam; PRO0082; Peptidase SB; I.

PRINTS; PRO0173; SUPTILISIN.

PROSTITE; PRO0171; P. domain; I.

SMART; SMO0261; FU; I.7.

PROSTITE; PRO0136; SUBTILASE ASP; FALSE NEG.

PROSTITE; PRO0137; SUBTILASE HIS; I.

PROSTITE; PRO0139; SUBTILASE HIS; I.
                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOPORMS A; B AND C).
                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9NJ15-1; Sequence=Displayed;
                                                                                                                           Proprotein convertage PC6-like) (aPC6).
EMBL; AF184615; AAF26300.1; -. EMBL; AF184616; AAF26301.1; -. EMBL; AF184617; AAF26302.1; -.
                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; Q99405; 1MPT.
                                                                                                                                                                       Branchiostoma.
NCBI_TaxID=7738;
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13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1504 Y--NCLSCPYGSKLGEGVCYPMCEEHBYYVEKTQICEECDNSCKTC---RGSTAHDCLSC 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 -----ALERIGMKQIGVCLSSCPSGYYGTRYPDI-NKCTKCKA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 HTMECVSIVH------CBVSEW-----NPWSPCTKKGKTCGPKRGTBTRVREII 181
                                                                                                                                                                                                                                                                      CLEAVAGE (AUTO-) (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCKAC...) (POTENTIAL).
N-LINKED (GLCKAC...) (POTENTIAL).
DDIILDRGECITSCOPGEYMDREKKCKACHPICKECSDEY
                                                                                                                                                                                                                                                                                                                                                                                                                                               DDTCTACNDGFILIDASSCEAGCP -> AENQNQASFCPFA
PREVSVLAELALGHLRYSLIDVPPQSNSPPDTVLGADRARL
TTATSAAGRCA (in isoform C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=VSP_005443.
CHPTCKRCSDEYDPUTCHONGFLLTDASSCEACCPPGQFL
HHGDDGSCHRECTTC -> IANCUPREDESWCDLVLENPC
VRRYFVKRCCGTCKLYMEDRPMRRGSSQPTQGRN (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 12.2%; Score 184.5; DB 1; Length 1696;
1 Similarity 22.7%; Pred. No. 8.2e-06;
64; Conservative 25; Mismatches 74; Indels 119; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 MHPNVSQGCQGCATCS--DYNGCLSCKPRLFF-------
                                                                                     POTENTIAL. PROPROTEIN CONVERTASE SUBTILISIN/KEXIN
Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;
Cleavage on pair of basic residues; Repeat; Alternative splicing;
Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P30432; Q24301;
01-APR-1993 (Rel. 25, Created)
28-FRB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Purin-like protease 2 precursor (BC 3.4.21.75) (Furin 2).
PURZ OR CG18734/CG4235.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                    CYS-RICH MOTIF (CRM) REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1344 1696 Missing (in isoform A).
/FTIGHVSP 005445.
1696 AA; 188410 MW; 281CBE1784257CBD CRC64;
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                                                                                                                                                                     POTENTIAL.
CYTOPLASMIC (POTENTIAL)
CATALYTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId=VSP 005442.
Missing (in isoform C).
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Best Local Similarity
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26
111
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TRANSMEM
DOMAIN
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CARBOHYD
VARSPLIC
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ACT_SITE
CARBOHYD
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DOMAIN
DOMAIN
SITE
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AMEMINGENETREEY,
Addmar No. Celniker S. B., Holl R. A., Brans C. A., Gocayne J. D.,
Addmar M.D., Celniker S. B., Holl R. A., Brans C. A., Gocayne J. D.,
B. Addman M.D., Celniker S. B., Li P. W., Hoskins R. A., Galle R. F.,
B. George R. A., Lewis S. B., Li P. W., Hoskins R. A., Galle R. F.,
B. George R. A., Lewis S. B., Richards S., Ashburner M., Henderson S. N.,
B. Brandon R. C., Rogers Y. H. C., Blazel R. G., Nelson C. R., Miklos G. L. G.,
Addring M. B. Basu A., Baxendale J., Bayraktaroglu L., Beasley E. M.,
B. Ballew R. M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E. M.,
B. Ballew R. M., Basu A., Baxendale J., Brokstein P., Blaibakov S.,
B. Ballew R. M., Basu A., Baxendale J., Brokstein P., Blaibakov S.,
B. Borkova D., Borchan M.R., Bouck J., Brokstein P., Blaibakov S.,
B. Burles K.C. Busam D. A., Buller H., Gadleu B., Center A., Chandra I.,
B. Delcher A., Deng Z., Mays A.D., Dew I., Diavies P.,
Cherry J. M., Cadley S., Dahlke C., Davenport L. B., Davies P.,
B. Durbin K.J. Bromes W., Dayan-Rocha S., Plaischmann W.,
R. Beblos B., Delcher A., Howland T. J., Herriars M., Houck J.,
B. Hostin D., Houston K. A., Howland T. J., Herriars M., M., Gabriellan A.B., Gabriellan R. Gabriellan A.B., Gabriellan A.B., Gabriellan A.B.,
Jalai M., Kalush F., Karpen G. H., Ke Z., Kanpison J. A., Kechun K. A.,
Jalai M., Kalush P., Rarpen G. H., Karvitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levierky A.A., Li J. H., Li Z., Liang Y., Lin X.,
Lasko P., Lei Y., Levierky A.A., Li J. H., Li Z., Liang Y., Lin X.,
Matteria B., Mount S.M., Muxphy B., Muxphy L., Muxny D.M., Nelson D.L.,
Reinert K., Nelson K.A., Nixon K., Nusakern D., Puri, V., Resen M.G.,
Reinert K., Saudaling A.C., Stapleton M., Stupski M. P.,
Spier E., Spradling A.C., Stapleton M., Stupski M. P.,
Wellyn K., Wassarman D.A., Weinercock G.M., Weissenbach J.,
Williams S.M., Woodage T., Wohley K., Wu D., Yang G., Zhu X., Smith H.O.,
Ritcher R., Myere B. W., Wolley K.C., Wu D., Yang G., Shith H.O.,
Ritcher R., Romer R., Rubin G., Stuper J., Shith W., Schue B.C., Stence 
                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=Oregon.*R. Tuebingen, and Iso-1;
MEDLINE=92381036, PubMed=1512259;
MEDLINE=92381036, PubMed=1512259;
Robiton N., Cremers J.W.M., Pauli I.G.L., Kurzik-Dumke U.,
Rentrop M., Gateff E.A.F., Leunissen J.A.M., van de Ven N.J.M.;
"Cloning and functional expression of Dfurin2, a subtilisin-like
proprotein processing enzyme of Drosophila melanogaster with multiple
repeats of a cysteine motif.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: Furin is likely to represent the ubiquitous endoprotease activity within constitutive secretory pathways and capable of cleavage at the RX(K/R)R consensus motif (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The Dfurz gene of Drosophila melanogaster: genetic organization, expression during embryogenesis, and pro-protein processing activity of its translational product Dfurin2.";
DNA Cell Biol. 14:223-234(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roebroek A.J.M., Ayoubi T.A.Y., Creemers J.W.M., Pauli I.G.L., van de Ven W.J.M.;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 267:17208-17215(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=1so-1;
MEDLINE=95186060; Pubmed=7880443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                NCBI_TaxID=7227;
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CATALYTIC ACTIVITY: Release of mature proteins from their proproteins by cleavage of Arg-Kaa-Yaa-Arg-1-Zaa bonds, where Xaa can be any amino acid and Yaa is Arg or Lys. Releases albumin, complement component C3 and von Willebrand factor from their

respective precursors. TISSUE SPECIFICITY: Transient expression in a subset of central

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nervous system neurons during embryonic stages 12-13. Expression in developing tracheal tree from stage 13 to end of embryonic
                        development.
--- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
--- SIMILARITY: Belongs to peptidase family S8. Purin subfamily.
                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00136; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS001318; SUBTILASE HIS; 1.
Hydrolase; Serine protease; Glycoprotein; Signal; Transmembrane; Multigene family; Zymogen; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
FURIN-LIKE PROTBASE 2.
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
10 X TANDEM REPEATS, CYS-RICH.
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3F9E749F0B021CF6 CRC64;
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InterPro; IPR006212; Furin repeat.
InterPro; IPR0019030; Grow Fac. Facep.
InterPro; IPR0019089; Peptidase S8.
InterPro; IPR0019884; Peptidase S8.
InterPro; IPR0019884; Peptidase S8.
InterPro; IPR0019020; Protease Intib.
Ffam; PF001483; P. proprotein; Z.
PRINTS; PR00723; SGBTILISIN.
PRODOM; PD0000717; P. domain; I.
SNART; SN00261; FU; IO.
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MBROPS; 808.049; -.
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                                                                     1037 HLHVID-LAVCLQPCPDGYFENS----RNRTCVP-----CEPNCASCQDHPEYCTSCDHH 1086
                                                                                             62 LPFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCP--NKNPCTKCKSGF 119
                                                                                                                                           120 YLHLGKCLLDNCPEGLEANNHTWECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRV-R 178
                                                5
                                               3 HLRLISWLPIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDY-NGCLSCKPR
                          Gaps
                                                                                                                                                                                                                                                                     PAC4 HUMAN STANDARD; PRT; 969 AA.
P29122; Q15099; Q15100; Q9UBG7; Q9UBJ1; Q9UBJ2; Q9UBJ7; Q9UBJ8; Q9UBJ9; Q15100; Q9UBG7; Q9UBJ1; Q9UBJ2; Q9VBJ7; Q9UBJ8; Q9VBJ9; Q9Y4H0; Q9YBH1; Q9UBC-1992 (Rel. 24, Created)
01-DBC-1992 (Rel. 24, Last sequence update)
15-MAR-2004 (Rel. 41, Last annotation update)
Paired basic amino acid Cleaving enzyme 4 precursor (BC 3.4.21.-)
(Subtilisin/kexin-like protease PACE4) (Subtilisin-like proprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Identification of novel cDNAs encoding human kexin-like protease
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                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tsuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H., Matsuda Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tsuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H., Matsuda Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of a second human subtilisin-like protease gene
                         53;
  Length 1679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOPORMS PACE4A-I AND PACE4B).
TISSUE=Hepetcoma, and Kidney.
MEDLINE=92075167; PubMed=1741956;
Kiefer M.C., Tucker J.E., Joh R., Landsberg K.E., Saltman D.,
 11.6%; Score 176.5; DB 1; Length 28.0%; Pred. No. 3e-05; ive 24; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification of a novel PACB4 isoform, PACB4B.";
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS PACE4E-I AND PACE4E-II).
TISSUE=Cerebellum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. 204:1381-1382(1994)
DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. Biophys. Res. Commun. 200:943-950(1994)
                                                                                                                                                                                                              1177 ECLONWI -----LNKRDKCIVSGSEGCSESE 1202
                                                                                                                                                                                          179 EIIQHPSAKGNLCPPTNETRKCTVQRKK-CQKGE 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM N.A. (ISOFORMS PACE4C AND PACE4D)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the fes/fps region of chromosome 15.";
DNA Cell Biol. 10:757-769(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95071480; PubMed=7980617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94235049; PubMed=8179631;
                        60; Conservative
                                                                                                                                                                                                                                                                                                                                                                      convertase 4) (SPC4)
PACE4.
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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Nagahama M., Taniguchi T., Hashimoto B., Imamaki A., Mori K.,
Nagahama M., Taniguchi T., Hashimoto B., Imamaki A., Mori K.,
Tsuji A., Matsuda Y.;
Tsuji A.
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MEDLINE-97335942; PubMed-9192737;
Mori K., Kii S., Tsuji A., Nagahama M., Imamaki A., Hayashi K.,
Akamatsu T., Nagamune H., Marsuda Y.;
A novel human PACE4 isoform, PACE4E is an active processing protease
containing a hydrophobic cluster at the carboxy terminus.";
J. Biochem. 121:941-948(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PACEAB-I AND PACEAB-II).
MEDIINE=98021085; PubMed=9378725;
TSuji A., Hine C., Tamai Y., Yonemoto K., Mori K., Yoshida S.,
Bando M., Sakai B., Mori K., Akamatsu T., Mareuda Y.;
"Genomic organization and alternative splicing of human PACE4 (SPC4),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mochring T.J.; "Mochype PACR4 is Ca2+-dependent and temperature-sensitive and "Employncease PACR4 is Ca2+-dependent and temperature secue the phenotype of a furin-deficient cell strain."; Biochem. J. 339:639-647(1999).
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Note=Probably enzymatically inactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS PACE4A-I; PACE4A-II; PACE4CS; PACE4D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhong M., Benjannet S., Lazure C., Munzer S., Seidah N.G., "Punctional analysis of human PACE4-A and PACE4-C isoforms: identification of a new PACE4-CS isoform.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99233559; PubMed-10215603;
Sucic J.F., Mochring J.M., Inocencio N.M., Luchini J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSP_005429;
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Note=Probably enzymatically inactive;
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Name=PACE4A-1; Synonyms=PACE4;
IsoId=P29122-1; Sequence=Displayed;
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IsoId=P29122-3; Sequence=VSP 005428, Note=Probably enzymatically inactive;
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Note=Probably enzymatically inactive;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTERNATIVE SPLICING (ISOFORM PACE4CS).
MEDLINE=97064242; PubMed=8906861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kexin-like processing endoprotease.";
J. Biochem. 122:438-452(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEBS Lett. 396:31-36(1996).
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44; Conservative
                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                       Similarity
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                                                                        Query Match
Best Local S:
Matches 44
                                                                                                                                                                                                                                                                                                                                RESULT 5
PCK5_RAT
ID PCK5_1
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                            Name=PACE4B-II;
IsoId=P29122-8; Sequence=VSP 005436, VSP 005437;
IsoId=P29122-8; Sequence=VSP 005436, VSP 005437;
TISSIGE SPECIPICITY: Rach PACE4-isoform exhibits a unique
placenta, lung, skeletal muscle, kidney, pancreas, but at
comparatively higher levels in the liver. PACE4A-II is at least
expressed in placenta. PACE4B was only found in the embryonic
expressed in placenta. PACE4B was isolated. PACE4C and PACE4D
expressed in placenta. PACE4B-II is expressed in cerebellum,
placenta and pituitary. PACE4B-II is at least present in
                                                                                                                                                                                           -1- DOWAIN: The propeptide domain acts as an intramolecular chaperone assisting the folding of the zymogen within the endoplasmic reticulum. Isoform PACR4D lacks the propeptide domain.
-1- SIMILARITY: Belongs to peptidase family S8.
-1- SIMILARITY: Contains 1 PLAC domain.
Name=PACE4B-I;
IsoId=P29122-7; Sequence=VSP_005437;
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AB001898; BAA21620.1;
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737 YPGDTAÁRKCRR-----CHKGCBTCSSRAATOCLSCR-RGFY-----HHQEMNT 779
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Dev. Biol. 181:268-283(1997).

-I- FUNCTION: Likely to represent a widespread endoprotease activity

-i- FUNCTION: Likely to represent a widespread endoprotease activity

within the constitutive and regulated secretory pathway. Capable

of cleavage at the RX(K/R)R consensus motif. May be responsible

for the maturation of gastrointestinal peptides. May be involved

in the callular proliferation of adrenal cortex via the activation

of growth factors.

-i- CATALYTIC ACTIVITY: Release of mature proteins from their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and peripheral tissues of
                                                                                                                                                                                                                                                                                                                                         19 YIGSQNASRGRRQRRMHPNVSQGCQGCATCSD--YNGCLSCKPRLFFALBRIGMKQIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P414II; Q62914;
01.NOV-1995 (Rel. 32, Created)
10.NOV-2001 (Rel. 43, Last annotation update)
15.MAR-2004 (Rel. 43, Last annotation update)
Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
(Proprotein convertase PC5) (Subtilisin/kexin-like protease PC5)
(Fregment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Adrenal gland;
MISDLINE-3342065, PubMed-8341687;
MISDLINE-3342066, PubMed-8341687;
MISSON STRUCTURE OF the mouse and rat subtiliain/kexin-like PC5: a candidate proprotein convertage expressed in endocrine and nonendocrine cells.";
Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Adrenal gland;
De Bie I., Marcinkiewicz M., Nakayama K., Lazure C., Seidah N.G.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97166043; PubMed=9013936;
Zheng M., Seidah N.G., Pintar J.B.;
"The developmental expression in the rat CNS and peripheral tiss
proteases PCS and PACE4 mRNAs: comparison with other proprotein
                                                                                                                                                                                                                                                                     39;
                                                                                                                                                                                    Length 969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM SHORT), AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                     54;
                                                                                                                                                                                         DB 1;
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                                                                                                                                                                                    11.4%; Score 173.5; DB: 28.8%; Pred. No. 2.9e-05; tive 16; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 ANNHIMECVSIVHCEVSEWNPWSPCTKKGKTCG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   838 FDSELIRCGECHH--------TCG 853
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EMBL; AB001901; BAA21624.1; JOINED.
EMBL; AB001902; BAA21624.1; JOINED.
EMBL; AB001903; BAA21624.1; JOINED.
EMBL; AB001904; BAA21624.1; JOINED.
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Name=PCSB; Synonyms=Long;
Name=PCSB; Synonyms=Long;
IsoId=P41413-1; Sequence=Displayed;
Name=PCSB; Synonyms=Long;
Name=PCSA; Synonyms=Long;
IsoId=P41413-2; Sequence=VSP 005440, VSP 005441;
IsoId=P41413-2; Sequence=VSP 005441;
IsoId=P41413-1; Sequence=VSP 005441;
IsoId=P41414-1-1; Sequence=VSP 005441;
IsoId=P41413-1; Sequence=VSP 005441;
IsoId=P41414-1-1; Sequence-VSP 005441;
IsoId=P41414-1-1-1; Sequence-VSP 005441; IsoId=P41414-1-1; Sequence-VSP 005441; IsoId=P41414-1-1; IsoId=P4141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
proproteins by cleavage of Arg-Xaa-Yaa-ARG-|-Zaa bonds, where Xaa can be any amino acid and Yaa is Arg or Lys.
SUBCELLULAR LOCATION: PC5A IS SECRETED THROUGH THE REGULATED SECRETORY PATHWAY. PC5B IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH EARLY ENDOSOMES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN: The propeptide domain acts as an intramolecular chaperone assisting the folding of the zymogen within the endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- DOMAIN: AC 1 and AC 2 (clusters of acidic amino acids) contain sorting information. AC 1 directs TGN localization and interacts with the TGN sorting protein PACS-1.
-!- SIMILARITY: Belongs to peptidase family S8.
-!- SIMILARITY: Contains 1 homo B/P domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R InterPro; IPR006212; Purin repeat.
R InterPro; IPR00209; Peptidase SB.
InterPro; IPR00209; Peptidase SB.
R InterPro; IPR002009; Peptidase SB.
R InterPro; IPR009020; Procease Inhib.
R Fam; PF01483; Purporotein; I.
R Probom; PD000717; P domain; 1.
R SWART; SW00261; FU; 6.
R PROSITE; PS00136; SUBTILASE ASP; 1.
R PROSITE; PS00137; SUBTILASE ASP; 1.
R PROSITE; PS00138; SUBTILASE SER; 1.
R PROSITE; PS00139; SUBTI
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BY SIMILARITY.
PROPROTEIN CONVERTASE SUBTILISIN/KEXIN
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CYTOPLASMIC (POTENTIAL).
CATALYTIC.
CHOMO B.
CYS-RICH MOTIF (CRM) REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                         Bvent=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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HSSP; Q99405; IMPT.
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11;
                                                                                                                                                                                                                                                                                                                                                                                                                      682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 VHCEVSEWNPWSPCTKKGKTC-GPKRGTETRVREIIQHPSAKGNLCPPTNETRKCTVQRK 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      740 ------GKCSENCKTCTGFHNCTE-----CKGGL---SLQGSRCSV--- 771
                                                                                                                                                                                                                                                                                                                                                                                            90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCK5 HUMAN STANDARD; PRT; 913 AA.
Q92824; Q13527;
16-CCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Proprotein convertase subtilisin/kexin type 5 precursor (BC 3.4.21.-)
Proprotein convertase PC5) (Subtilisin/kexin-like protease PC5) (PC6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   640 PECSEVGCDGPGPDHCTDCLHYHYKLKNNTR------ICVSSCPPGHP---H
                                                                                                                                                                                                                                                                                                                                                                                           36 PNVSQ-GCQG----GCATCSDYNGCLSCKPRLPPALERIGMKQIGVCLSSCPSGYYGTRY
                                                                                                                                                                                                                                                                                                                                                              54; Indels 58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miranda L., Wolf J., Pichuantes S., Duke R., Franzusoff A.; "Isolation of the human PCG gene encoding the putative host protease for HIV-1 gp160 processing in CD4+ T lymphocytes."; Proc. Natl. Acad. Sci. U.S.A. 93:7695-7700(1996).
                                                                                                                                                                                                                    ATERSWAEGGPCMLVKKNNLCQRKVLQQLCCKTCTPQG
                                                     CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lu Y., Duke R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                11.1%; Score 168; DB 1; Length 1877; 26.3%; Pred. No. 0.00014; ive 25; Mismatches 54; Indels 58
                                                                                                                                                                                                                                                                                                       MW; 890955DC60534444 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Franzusoff A., Miranda L., Wolf J., Pichuantes S., Lu Y. Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                       Missing (In isoform PC5A). / FTId=VSP_005441.
AC 1.
AC 2.
CELRAVAGE (AUTO-) (BY S.
CELL ATTACHMENT SITE (CHARGE RELAY SYSTEM (B.
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/Prid=VSP 00
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MEDLINE=96353880; PubMed=8755538;
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 1844
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                                                                                                                                                                                                                                                                             916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS: SUB-076; -.

MEROPS: SUB-076; -.

MEROPS: SUB-076; -.

MIM; 600489; -. C:extracellular space; TAS.

MIM; 6000452; F:serine-type endopepidase activity; TAS.

GO; GO:0005263; F:serine-type endopepidase activity; TAS.

GO; GO:0005269; P:portocolysis and peptidolysis; TAS.

MIREPO: IPR006219; Peptidase SB.

InterPro: IPR006219; Peptidase SB.

InterPro: IPR006219; Peptidase SB.

InterPro: IPR009209; Peptidase SB.

InterPro: IPR00923; Peptidase SB.

InterPro: IPR0923; INTERATY.

InterPro: IPR0923; PEPTIDAITY.

InterPro: IPR0923; P
Submitted (FEB-1996) to the EWBL/GenBank/DDBJ databases.
Submitted (FEB-1996) to represent a widespread endoprotease activity
Inthin the constitutive and regulated secretory pathway. Capable
of Cleavage at the EX(K/R)R consensus motif.

CATALYTIC ACTIVITY: Release of mature proteins from their
proproteins by cleavage of Arg-Xaa-Yaa-ARG-|-Zaa bonds, where Xaa
can be any amino acid and Yaa is Arg or Lys.

SUBCELLULAR LOCATION: Secreted (By similarity).

ALTERNATIVE PRODUCTS:
EVent=Alternative splicing; Named isoforms=1;
                                                                                                                                                                                                                                                                                                                       IsoId=Q92824-1; Sequence=Displayed; IsSUE SPECIFICITY: Expressed in T-lymphocytes. DOMAIN: The propeptide domain acts as an intramolecular chaperone assisting the folding of the zymogen within the endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLEAVAGE (AUTO-) (BY SIMILARITY).
CELL ATTACHMENT SITE (POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYS-RICH MOTIF (CRM) REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to peptidase family S8.
-!- SIMILARITY: Contains 1 homo B/P domain.
-!- SIMILARITY: Contains 1 PLAC domain.
                                                                                                                                                                                                                                                                            Comment=2 isoforms may be produced;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE 5.
CATALYTIC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U56387; AAC50643.2; -. EMBL; U49114; AAA91807.1; -. PIR; G02428, G02428, HSSP; Q99405; IMPT.
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79 SSCPSG-YYGTRYPDINKCTKCKADCDICPNKNPCTKCKSGPYLHLGKCLDNCPEGLEAN 137
                                                                                                                                                                                                                                                                                                             722 THCPDGSYQDTKK---NLCRKCSENCKTCTBFHNCTECRDGLSLQGSRCSVSCEDGRYFN 778
                                                                                                                                                                                                                                                                                                                                               138 NHTMR-----NPWSPCTKK 163
                                                                                                                                                                                                                                                                                                                                                                                 779 GODCOPCHRFCATCAGAGADGCINCTEGYFMEDGRCVQSCSISYYPDHSSENGYKSCKKC 838
                                                                                                                                                                                                                                                                                                                                                                                                                  164 GKTC-----GFKRGTE-----TRVREIIQHPSAKGNLCPPTNETRKCTV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22388257; PubMed=12477932;

A Strausberg R.L. Feingold E.A., Grouse L.H., Derge J.G.,

A Riamener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F.,

Bottchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S.Y., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Butfard G.G.,

Rakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
                                                                                                                                                                                                        21 GSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNG--CLSCKPRLFFALERIGMKQIGVCL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99215557; PubMed=10201374;
Hsieh J.-C., Kodjabachian L., Rebbert M.L., Rattner A.,
Smallwood P.M., Sonso C.H., Nusse R., Dawid I.B., Nathans J.,
Rallwood P.M., Sonso C.H., Nusse R., Dawid I.B., Nathans J.,
"A new secreted protein that binds to Wnt proteins and inhibits their
                                                                                                                                                                       78; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
(POTENTIAL)
(POTENTIAL)
                                                                                                                                     10.7%; Score 162; DB 1; Length 913; 22.3%; Pred. No. 0.00018; ive 33; Mismatches 81; Indels 7
                              118 S -> F (IN REF. 3).
121 V -> A (IN REF. 3).
131 R -> A (IN REF. 3).
131 R -> A (IN REF. 3).
101775 MW; 21389264CAD7546C CRC64;
 (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0915W5; Q8WVG4;
16-OCT-2001 (Rel. 40, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Wht inhibitory factor 1 precursor (WIF-1).
                   (GLCNAC
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 N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activities.";
Nature 398:431-436(1999).
                                                                                                                                                                         55; Conservative
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Best Local Similarity
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COGCCAT---CSDYNGC-----LSCKPRLFPALERIGMKQIGVCLSS----C
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
WAT inhibitory factor 1 precursor (WIF-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P00740; IRDM.
InterPro; IPR006209; EGF like.
InterPro; IPR006210; IRGF.
InterPro; IPR00249; Laminin_EGF.
InterPro; IPR003306; WIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF122924; AAD25404.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00008; BGF; 5.
Pfam; PF02019; WIF; 1.
PRINTS; PR00001; BGPLAMININ.
SWART; SMO0181; BGF; 4.
SWART; SMO0469; WIF; 1.
PROSITE; PS00022; BGF_1; 5.
                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                    Kenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8355;
                                                                                                                                                    E 247
                                                                                                                                                                     374 B 374
                                                                                                                                                                                                                                                                                                                                                                                              activities.";
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AC Q9W6F8;
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                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83;
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.5%; Score 158.5; DB 1; Length 379; 24.9%; Pred. No. 0.00014; Live 26; Mismatches 72; Indels 83.
                                                                                                                                                                                                                                                                                         PRINTS: PRO0011; BGFLAMININ.
SMART; SM00181; BGF: 5.
SMART; SM00469; WIF; 1.
SMOSITE; PS00022; BGF 1; 5.
PROSITE; PS50026; BGF 2; 4.
PROSITE; PS5004; WIF; 1.
Repeat; BGF-1; WIF; 1.
Repeat; BGF-1; WIF; 1.
Repeat; BGF-1; WIF; 1.
Repeat; BGF-1; WIF; 1.
SEG-1; WIF; 1.
SEG-1; WIF; 1.
SEG-1; WIF; 1.
SEG-1; WIF; 1.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K -> Q (IN REF. 1).
Q -> L (IN REF. 1).
32BC54D60529EP96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         WNT INHIBITORY FACTOR 1. WIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. .
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BGP-LIKB 2.
BGP-LIKB 3.
BGP-LIKB 4.
BGP-LIKB 5.
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                                                                                                                                                                                                                                       InterPro; IPR006209; EGF_like.
InterPro; IPR006210; IEGF.
InterPro; IPR002049; Laminin_EGP.
InterPro; IPR003306; WIF.
                                                                                                                                                                                EMBL; AF122922; AAD25402.1; -. EMBL; BC018037; AAH18037.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41528 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                            HSSP; P00743; 1CCP.
Genew; HGNC:18081; WIF1.
                                                                                                                                                                                                                                                                              Pfam; PF00008; EGF; 5.
Pfam; PF02019; WIF; 1.
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379 AA;
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tes 60; Conserv
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262
273
278
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                              82 PSGYYGTRYPDINKCTKC-KADCD-TCFNKNPCTKCKSGPYLHLGKCLDNCPEGLEANNH 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 IMBCVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQHPSAKGNLCPP---- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CERISKCP--QPCRNGGKCIG---KSKCKCSKGYQGDLCSKPVCEPGCGAHG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 -TNETRKCTVORKKCOKGERGKKGRERKRK-----KPNKGESKEAIPDSKSLESSKEIP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :| || :| | | :: | | :: | | 3.3 | 3.13 | 1.14 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15
182 CPGGCRNGGPCNERRICECPDGFHGPHCEKALCTPRCMNG------GLCVTPGFCIC 232
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-I- FUNCTION: Binds to WNT proteins and inhibits their activities. May be involved in mesoderm segmentation.

-I- SUBCELLULAR LOCATION: Scretched.

-I- TISSUB SPECIFICITY: During somatogenesis, expressed predominantly in unsegmented paraxial presomitic mesoderm and, to a much lesser extent, in newly segmented somites.

-I- DEVELOPMENTAL STAGE: First expressed at neurula stages.

-I- SIMILARITY: Contains 1 WIF domains.
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=99215557; PubMed=10201374;
Haieh J.-C., Kodjabachian L., Rebbert M.L., Rattner A.,
Smallwood P.M., Samos C.H., Nusse R., Dawid I.B., Nathans J.;
"A new secreted protein that binds to Wnt proteins and inhibits their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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DR InterPro; IPR002829; Peptidase S8.

InterPro; IPR002884; Peptidase S8.

DR InterPro; IPR002884; Peptidase S8.

DR InterPro; IPR003020; Protease Inhib.

DR Pfam; PP00482; Peptidase S8.

DR Pfam; PP00482; Peptidase S8.

DR Pfam; PR00521; SubTiliSiN.

DR ProDom; PR00521; Peptidase S8.

DR PR05TE; PS5090; PLAC; 1.

DR PR05TE; PS00136; SubTiliASE ASP; 1.

RR05TE; PS00137; SubTiliASE HIS; 1.

RR05TE; PS00137; SubTiliASE HIS; 1.

RR05TE; PS00138; SubTili
                                                                                           19 YIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYN--GCLSCKPRLFFALBRIGMKQIGV
                           pitultary and regulated by thyroid status.",
Endocrinology 135:1178-1185(1994).
--- FUNCTION: Likely to represent an endoprotease activity within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAIRED BASIC AMINO ACID CLEAVING ENZYME
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(BY SIMILARITY).
(BY SIMILARITY).
       "PACE4: a subtilisin-like endoprotease prevalent in the anterior
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(GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
557C33705C8 CRC64;
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CYS-RICH MOTIF (CRM) REGION.
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CELL ATTACHENT SITE (E
CHARGE RELAY SYSTEM (B)
CHARGE RELAY SYSTEM (B)
CHARGE RELAY SYSTEM (B)
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                                                                                                                                                                                                                                                                                                                                                                                    -i-SIMILARITY: Belongs to peptidase family S8.-i-SIMILARITY: Contains 1 homo B/P domain.-i-SIMILARITY: Contains 1 PLAC domain.
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N-LINKED (GLCNAC.
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Matches 51; Conservative
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HSSP; Q99405; 1MPT.
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937 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CQGGCAT---CSDYNGC-----LSCKPRLFFALERICMKQIGVC----LSSC
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAR-2004 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Paired basic amino acid cleaving enzyme 4 precursor (BC 3.4.21.-)
(Subtilisin/kexin-like protease PACE4) (Subtilisin-like proprotein convertase 4) (SPC4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 VQRKKCQKGERGKKGRERKRK-----KPNKGESKEAIPDSKSLESSKEIPE
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85; Indels
                                                           ; WIF; 1.
domain; Signal; Developmental protein;
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41071 MW; R26F973B0F00ACF8 CRC64;
                                                                                                                                               WNT INHIBITORY FACTOR 1.
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EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 4.
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PROSITE; PS50026; EGF 2; 5. PROSITE; PS50026; EGF 3; 4. PROSITE; PS50844; WIF; 1. Repeat; EGF-like domain: Sir sirnal.
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                                                                                                   Wnt signaling pathway.
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063415;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  weed by Housepite institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
CLSSCPSGYYGTRYPDINKCTKCKADCDTCFNK-NFCTKCKSGFYLHLGKCLDNCPEGLE 135
                853
                                                           ----VSIVHCEVS----EWNPWSPCTKKGKTCGFXRGTETR
                                                                                      806 PDSELIRCGECHHTCRTCVGPSREECIHCAKSFHFQDWKCVPACGE-----GF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruiz i Altaba A., Cox C., Jessell T.M., Klar A.;
"Ectopic neural expression of a floor plate marker in frog embryos injected with the midline transcription factor Pintallavis.", Proc. Natl. Acad. Sci. U.S.A. 90:8268-8272(1993).
-!- FUNCTION: Promotes the attachment of spinal cord and sensory neuron cells and the outgrowth of neurites in vitro. May contribute to the growth and guidance of axons in both the spinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cord and the PNS.
--- SUBCELLUAR LOCATION: Secreted.
--- TISSUB SPRCIPICITY: Expressed at high levels in the floor plate.
--- SIMILARITY: Contains 6 TSP type-1 domains.
                                                                                                                                                                                                                                                                                                                        Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                      177 VREIIQHPSAKGNLCPPTNETRKCTVQRKKCQKGER 212
                                                                                                                                                   ----YPEEMPGL --PHKVCRRCDENCLSCEGSSR 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 156; DB 1;
Pred. No. 0.00044;
                                                                                                                                                                                                                                                           01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last Bequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell adhesion.
                                                                                                                                                                                                                                  803 AA
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TSP TYPE-1 1.
TSP TYPE-1 2.
TSP TYPE-1 3.
TSP TYPE-1 4.
TSP TYPE-1 5.
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MEDLINE-93376785; PubMed-8367492;
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InterPro; IPR000884; TSP1.
Pfam; PP02014; Reeler; 1.
Pfam; PR00090; tsp 1; 6.
SMART; SM0209; TSP1; 6.
PROSITE; PS00092; TSP1; 6.
Glycoprotein; Signal; Repeat; 1.
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24.6%;
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                                                                                                                                                                                                                                STANDARD;
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677
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                                                           136 ANNHTMEC--
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                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8355;
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CARBOHYD
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Length 803;

Query Match Best Local Similarity

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                                                         656 CALPECP--ISCELTEMSYMSEC---NKSCG--KGHMIRTRMITMEPQFGGAVCPETVQR
                                    38 VSQGCQGGCATCSDYNGCLSCKPRLFFALRRIGMKQIGVCLSSCPS--GYYGTRYPDINK
                                                                                                     96 C--TKCK------ADCDTCFNKNPCTKCKSGFYLHLGKCLDNCPEGLEANN---
                                                                                                                                                                           139 -HTMECVSIVHCEVSEMNPWSPCTKKGKTCGPKRGTETRVREIIQHPSAKGNLCPPTWET
                                                                                                                                                                                                                                                                   and adult
 Gapa
                                                                                                                                                                                                                                                                                                                                                                     NTC2 MOUSE STANDARD; PRT; 2470 AA.
035516; Q06008; Q60941;
28-FRB-2003 (Rel. 41, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Neurogenic locus notch homolog protein 2 precursor (Notch 2) (Motch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hamada Y., Kadokawa Y., Okabe M., Ikawa M., Coleman J.R., Tsujimoto Y.; Kadokawa Y., Okabe M., Ikawa M., Coleman J.R., "Nutation in ankyrin repeats of the mouse Notch2 gene induces early embryonic lethality."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CS7BL/6; TISSUB-Thymus;
Hamada Y., Higuchi M., Tsujimoto Y.;
"Complete amino acid sequence and mutliform transcripts encoded by
single copy of mouse Notch2 gene.";
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1765-2153 FROM N.A.
MEDLINE-97075110; PubMed-8917536;
Milner L.A., Bigas A., Kopan R., Brashem-Stein C., Bernstein I.D.,
                                                                                                                                                                                                                                                 198 RKCTVQRKKCQKGERGKKGRERKRKKPNKGESKEAIPDSKSLESSKEIPEQRENKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       æ
52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-95333893; PubMed-7609614;
Higuchi M., Kiyama H., Hayakawa T., Hamada Y., Teujimoto Y.;
"Differential expression of Notchl and Notch2 in developing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1699.
MEDLINE-21523956; PubMed-11518718;
 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Martin D.I.;
"Inhibition of granulocytic differentiation by mNo
Proc. Natl. Acad. Sci. U.S.A. 93:13014-13019(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENTAL STAGE, AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouse brain.";
Brain Res. Mol. Brain Res. 29:263-272(1995).
 35, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 316-1518 FROM N.A.
STRAIN-C57BL/6 X CBA; TISSUE-Embryo;
MEDLINE-93178563; PubMed=8440332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99396706; PubMed=10393120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wide variety of tissues.";
Exp. Cell Res. 204:364-372(1993)
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
 58,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTCH2
                                                                                                                                                                                                                                                                                                                                                        NTC2_MOUSE
                                                                                                                                                                                                                                                                                                                                       RESULT 11
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MEDLINE-21374376; PubMed-11459941;
MEDLINE-2140 Notch family members.";
The Conservation of the blochemical mechanisms of signal transduction and angered; Jagged, Sci. U.S.A. 98:9026-9031(2001).

The Committee of the Sci. U.S.A. 98:9026-9031(2001).

The Committee of the committee cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus.

The Committee of the similarity of differentiation, proliferation and apoptotic programs (By similarity). May play an essential role in specification and/or differentiation.

The Specification and/or differentiation.

The Strum of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bonds.
SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus.
ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
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EMBL; X68279; CAA48340.1; -.
EMBL; W68279; CAA48340.1; -.
EMBL; U31881; AA57524.1; -.
EMBL; A49175, A49175.
HSSP; P16109; 1FSB.
MGD; MGI:97364; Notch2.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0005511; P:morphogenesis of an epithelial sheet; IMP.
GO; GO:0007219; P:N signaling pathway; IC.
Saxena M.T., Schroeter B.H., Mumm J.S., Kopan R.; *Murine notch homologs (N1-4) undergo presenilin-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- PTM: Piosphorylated.
-i- SIMILARITY: Belongs to the NOTCH family.
-i- SIMILARITY: Contains 35 BGP-like domains.
-i- SIMILARITY: Contains 2 Lin/Notch repeats.
-i- SIMILARITY: Contains 6 ANK repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=035516-1; Sequence=Displayed;
                                                proteclysis.";
J. Biol. Chem. 276:40268-40273(2001)
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CYTOPLASMIC (POTENTIAL).
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EGF-LIKE 4.
EGF-LIKE 4.
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NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor; Transcription regulation; Activator; Differentiation; Developmental protein; Repeat; ANK repeat; EGF-like domain; Transmembrane; Glycoprotein; Signal; Phosphorylation; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTCH EXTRACELLULAR TRUNCATION NOTCH INTRACELLULAR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL)
          InterPro; IPR000152; ABX hydroxyl_S. InterPro; IPR000152; ABX hydroxyl_S. InterPro; IPR000142; BGF_2. InterPro; IPR0010481; BGF_2. InterPro; IPR0010481; BGF_II. InterPro; IPR001049; BGF_II. InterPro; IPR001049; BGF_II. BGF. InterPro; IPR001049; BGF_II. BGF. InterPro; IPR001049; BGF_34. Pfam; PF00006; motch; 2. Pfam; PF00006; motch; 2. Ping; PR00104; BGF134. PRNTS; PR0011; BGF1AMININ. PRINTS; PR0011; BGF1AMININ. PRINTS; PR00125; NOTCH. SMART; SM00248; ANK; 6. SMART; SM00049; ML; 3. SMART; SM00179; BGF_CA; 23. SMART; SM0004; ML; 3. PROSITE; PS01081; MR REPEAT; 4. PROSITE; PS01082; BGF_2; 33. PROSITE; PS01186; BGF_2; 33. PROSITE; PS01186; BGF_2; 33. PROSITE; PS01186; BGF_2; 33. PROSITE; PS01187; BGF_2; 33. PROSITE; PS01187; BGF_2; 33.
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not heart.
--- DBVELOPMENTAL STAGE: Expressed in the embryonic ventricular zone, the postnatal ependymal cells, and the choroid plexus throughout embryonic and postnatal development.
--- PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proceolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a Cterminal fragment N(TM) and a N-terminal fragment N(TM) and a N-terminal fragment N(TM) and a notemediate fragment (TACE) to yield a membrane associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presentlin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=035516-2; Sequence=VSP_001405; Note=No experimental confirmation available; TISSUE SPECIFICITY: Expressed in the brain, liver, kidney, neuroepithelia, somites, optic vesicles and branchial arches, but
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(POTENTIAL). (POTENTIAL). (POTENTIAL). (POTENTIAL). (POTENTIAL). (POTENTIAL).

(POTENTIAL) .

(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).

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-1- SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                            EMBL; L29232; AAA41392.1; -.
EMBL; M27293; AAA41384.1; -.
HSSP; P06213; 11RK.
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1275
1014
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12;
                                                                                                                          983 ENNIDECTE----SSCPNGGTCVDGINSPSCLCPVGPTGPPCLHDINECSSNPCLNAGT 1037
                                                                                                                                                        126 CLDN------CPEGLEANNHTMECVSIVH-CEVSEWNPWSPCTKKGKTCGFKRGTETRV 177
                                                                               945 QTDMNBCLSEPCKNG-GTCSDYVNSYTC------TCPAGFHGVHC 982
                                                                                                       91 P-DINKCTKCKADCDTCFNKNFC------TKCKSGFYLHLGK 125
                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYCOSINE Phosphate.
SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-BINDING DOMAIN, WHILE THE BETA CHAIN CARRIES THE KINASE DOMAIN. SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F
                                                                  31 ORRMHPNVSQGCQGCATCSDYNGCLSCKPRLFFALERIGMKQIGVCLSSCPSGYYGTRY
                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                53; Indels 89; Gaps
                                                                                                                                                                                                                                                                                                                                                                                               Du J., Delafontaine P.; "Inhibition of vascular smooth muscle cell growth through antisense transcription of a rat insulin-like growth factor I receptor CDNA."; Circ. Res. 76:963-972(195).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Developmental regulation of the rat insulin-like growth factor I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Werner H., Woloschak M., Adamo M., Shen-Orr Z., Roberts C.T. Jr.,
                                                                                                                                                                                                                                                                      01-MAR-1992 (Rel. 21, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-PBB-2003 (Rel. 41, Last annotation update)
Insulin-like growth factor I receptor precursor (BC 2.7.1.112)
                              DB 1; Length 2470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 913-1017 FROM N.A.
MEDLINE=92412145; PubMed=1530648;
Kurachi H., Jobo K., Ohta M., Kawasaki T., Itoh N.;
Ha new member of the insulin receptor family, insulin receptor-related receptor, is expressed preferentially in the
                                                                                                                                                                                                     1077 ---VÓEKARPHCLCPPGWDGAYCDVLNVSCKAAALQKG 1111
                                                                                                                                                                                   178 REIIQHPSAKGNLCPPTNETRKCTVQRKKC-----QKG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor gene.";
Proc. Natl. Acad. Sci. U.S.A. 86:7451-7455(1989)
                           ch 9.9%; Score 150.5; DB 1 Similarity 24.3%; Pred. No. 0.0031; 53; Conservative 23; Mismatches 5
                                                                                                                                                                                                                                                    PRT; 1370 AA
 LIN/NOTCH 2.
ANK 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Sprague-Dawley;
MEDLINE=90017496; Pubmed=2477843;
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95277910; PubMed=7758167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-364 FROM N.A.
                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor subfamily
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leroith D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kidney.";
                             Query Match
Best Local S:
Matches 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALPHA-CHAIN.
INSULIN-LIKE GROWTH FACTOR I RECEPTOR,
                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000494; EGRR L domain.

InterPro; IPR000494; EGRR L domain.

InterPro; IPR000494; EGRR L domain.

InterPro; IPR000404; Pal III-like.

InterPro; IPR000401; Pal III-like.

InterPro; IPR000511; Purin repeat.

InterPro; IPR000512; Purin repeat.

InterPro; IPR000401; EcceptityTkinsI.

InterPro; IPR000401; ReceptityTkinsI.

InterPro; IPR000401; Fort Kinase.

INTERPRO; ER000401; Fort Kinase; I.

INTERPRO; ER000401; Fort Kinase; I.

INTERPRO; IPR000401; Fort II.

INTERPRO; IPR000401; INTERINASE ATP; I.

INTERPRO; IPR00109; FROTEIN KINASE ATP; I.

INTERPRO; INTERPRO;
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InterPro; IPR008297; Notch.

R InterPro; IPR008809; Notch.

R Ffam; PP00021; ank; 6.

Pfam; PP00021; ank; 6.

R Pfam; PP00021; ank; 6.

R Pfam; PP00021; ank; 6.

R Pfam; PP000219; Notch; 1.

R PRINTS; PR001010; EGFLAMININ.

R RINTS; PR00101; EGFLAMININ.

R RINTS; PR0010227; NOTCH.

R SWART; SW00014; ANK; ALPARAT; SW00014; ANK REPEAT; A.

R SWART; SW00004; NL; 2.

R ROSITE; PS00010; ASX HYDROXYL; 23.

R ROSITE; PS00106; ASX HYDROXYL; 23.

R ROSITE; PS00106; EGF 2; 29.

R ROSITE; PS010187; EGF 2; 29.

R ROSITE; PS01187; EGF
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                                                                                                                  ch
1 Similarity 26.7%; Pred. No. 0.0023;
47; Conservative 17; Mismatches 46; Indels 66; Gaps 11;
                                                                                                                                                                                                                                                          276 ------CVDRDFCANIPNAESSDSDGFVIHDGBCAQECPSGFIRNSTQSMYC 321
                                                                                                                                                                                                92 DINKCTKCKADCDTCFNKNPCTKC-----KSGPYLHLGKCLDNCPEGLEANN-HTMEC 143
                                                                                                                                                                               35 HPNVSQGCQGGCATCSDYNGCLSCKPRLPPALERIGWKQIGVCLSSCPSGYY---GTRYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kintner C.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Belongs to the NOTCH family.
-!- SIMILARITY: Contains 36 EGP-like domains.
-!- SIMILARITY: Contains 3 Lin/Notch repeats.
-!- SIMILARITY: Contains 6 ANK repeats.
                                                                                                                                                                                                                                                                                                  144 VSIVHCEVSEWNPWSPCTKKCKTCGPKRGTETRVREIIQHPSA------KGNL 190
                                                                                                                                                                                                                                                                                                                               322 IP---CE------GPCP---KVCG---DEEKKTKTIDSVTSAQMLQGCTILKGNL 361
    757 757 N-LINKED (GLCNAC. ..) (POTENTIAL).
755 755 N-LINKED (GLCNAC. ..) (POTENTIAL).
901 901 N-LINKED (GLCNAC. ..) (POTENTIAL).
914 914 N-LINKED (GLCNAC. ..) (POTENTIAL).
116 1166 PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
985 986 AD -> PY (IN REF. 3).
1370 AA; 155395 MY, A5946897A41CB145 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia, Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1991 (Rel. 18, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neurogenic locus notch protein homolog precursor (XOTCH protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=90385285; PubMed=2402639;
MEDLINE=90385285; PubMed=2402639;
"Xotch, the Xenopus homolog of Drosophila notch.";
"Xotech, the Xenopus homolog of Drosophila notch.";
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[2]
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InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR00042; BGF_2.
InterPro; IPR001881; BGF_Ca.
InterPro; IPR001438; BGF_II.
InterPro; IPR006209; BGF_II.
InterPro; IPR002049; Laminin_BGF.
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     TALLINGS.

-1. DEVELOPMENTAL STACE: Expressed in the brain during B14 and B17.

-1. DEVELOPMENTAL STACE: Expressed in the brain during B14 and B17.

-1. PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma embrane to yield an active, ligand-accessible form. Cleavage results in a Cterminal fragment N(TM) and a N-terminal fragment N(RC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presentil in dependent gamma-secretase to release a cleaved by presentil in dependent gamma-secretase to release a containing the intracellular domain (NICD) from the membrane (By similarity).

-1. SIMILARITY: Contains 3 bgP-like domains.

-1. SIMILARITY: Contains 2 Lin/Notch repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                            bonds (By similarity).

SUBCELLUIAR LOCATION: Type I membrane protein. Following
proteolytical processing NICD is translocated to the nucleus.
TISSUE SPECIFICITY: Highly expressed in the spleen and choroid
plexus in the brain. Expressed in postnatal central nervous system
(CNS) germinal zones and, in early postnatal life, within numerous
cells throughout the CNS. It is more highly localized to
ventricular germinal zones. Also found in the heart, liver and
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  development, probably in some aspect of cell specification and/or differentiation (By similarity). SUBDNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide
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SIGNAL

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InterPro; IPR001519; Ask hydroxyl_S.
InterPro; IPR0010152; Ask hydroxyl_S.
InterPro; IPR0010181; BGF_G.
InterPro; IPR0010181; BGF_II.
InterPro; IPR0010181; BGF_III.
InterPro; IPR0002049; LamInin_BGF.
InterPro; IPR0002049; LamInin_BGF.
InterPro; IPR0002049; Notch_dom.
Pfam; PF0001023; ank; 6.
Pfam; PF0001023; ank; 6.
Pfam; PF0001023; ank; 6.
Pfam; PF0001023; Notch; 1.
PRINTS; PR000101; BGFBLOOD.
PRINTS; PR00011; BGFBLOOD.
PRINTS; PR00011; BGFLAMININ.
SWART; SW00179; EGF_CA; 24.
SWART; SW00179; EGF_CA; 24.
PROSITE; PS000101; ANK_REPEAT; 4.
PROSITE; PS000101; ANK_REPEAT; 4.
PROSITE; PS000101; ANK_REPEAT; 2.
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PS01186; EGF_2; 26.
PS50026; EGF_3; 35.
PS01187; EGF_CA; 22.
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PIR; A49128; A49128.
HSSP; P00743; ICCF.
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            Thacker C., Srayko M., Rose A.M.; "Mutational analysis of bli-4/kpc-4 reveals critical residues required for proprotein convertase function in C. elegans."; Gene 252:15-25(2000).
                                                                                                                                                                                                                                                        PROSITE; PS00136; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
Hydrolase; Serine protease; Glycoprotein; Calcium-binding; Zymogen; Transmembrane; Signal; Alternative splicing.
1 20 POTENTIAL.
                                                             -I- FUNCTION: The Kex2/subtilisin-like proteinase activity of this enzyme is required for the normal production of adult cuticle. There is functional redundancy between the isoforms. Vital for embryonic and larval development.
-I- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; 808.031; --.
WormPep; KO4F10.4a; CE11728.
WormPep; KO4F10.4b; CE11730.
WormPep; KO4F10.4c; CE11732.
WormPep; KO4F10.4c; CE11734.
WormPep; KO4F10.6c; CE11734.
GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0004552; F:setine-type endopeptidase activity; NAS.
GO; GO:0007592; P:cuticle biosynthesis (sensu Invertebrata); IMP.
                                                                                                                                                                  Name=A; Synonyms=a;
IsoId=P51559-2; Sequence=VSP_005416, VSP_005419;
                                                                                                                                                                                             Name=B; Synonyms=b;
IsoId=P51559-3; Sequence=VSP_005418, VSP_005421;
                                                                                                                                                                                                                       Name=C; Synonyms=c;
IsoId=P51559-4; Sequence=VSP_005422, VSP_005423;
                                                                                                                                                                                                                                                                                                                                                                                          shown due to erroneous gene model prediction.
                                                                                                                                         Name=D; Synonyms=d;
IsoId=P51559-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L29438; AAA98750.1; ALT_FRAME.
EMBL; L29440; AAA98751.1; ALT_FRAME.
EMBL; APO39719; AAB96753.1; ALT_FRAME.
EMBL; APO39719; AAB96753.1; ---
EMBL; APO39719; AAB96753.1; ---
EMBL; APO39719; AAB96755.1; ALT_SEQ.
EMBL; APO39719; AAB96755.1; ---
EMBL; APO39719; AAB96755.1; ---
EMBL; APO39719; AAB96756.1; ---
EMBL; APO39719; AAB96756.1; ---
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InterPro; IPR009030; Grow fac recep.
InterPro; IPR002089; Peptidase_S8.
InterPro; IPR002884; Peptidase_S8.
InterPro; IPR009020; Protease Inhib.
Pfam; PF01483; P_proprotein; I.
Pfam; PF00082; Peptidase_S8; I.
PRINTS; PR000723; SUBTILISIN.
Probom; P000721; P domain; I.
SMART; SM00261; FU; 3.
MEDLINE=20363723; PubMed=10903434;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                126 CLD-----NCPEGLEANNHTMECVSIVH-CEVSEWNPWSPCTKKGKTCGFKRGTETRV 177
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                                                                                                                                                                                                                                                                                                                                                           947 QTDMNECLSEPCROG-GTCSDYVNSYTC-----TCPAGPHGVHC
                                                                                                                                                                                                                                                                                                                                                                                                            31 QRRMHPNVSQGCQGGCATCSDYNGCLSCKPRLFFALERIGMKQIGVCLSSCPSGYYGTRY
                                                                                                                                                                                                                                                                                                                  89; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BL14_CAEEL STANDARD; PRT; 943 AA.
P51559; O44762; O44763; O44766; O41766; O1-COT-1996 (Rel. 34, Created)
28-PSB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Endoprotease bli-4 precursor (EC 3.4.21.-) (Blisterase) (Blistered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thacker C., Peters K.W., Srayko M., Rose A.M.;
"The bli-4 locus of Caenorhabditis elegans encodes structurally distinct kex2/aubtilisin-like endoproteases essential for early development and audit morphology.";
Genes Dev. 9:956-971(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 2471;
                                                                                                                                                                                                                                                                            Score 147.5; DB 1; ucus-
Pred. No. 0.005;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1080 ----QEKARPRCLCPPGWDGAYCDVLNVSCKAAALQKG 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 REIIQHPSAKGNLCPPTNETRKCTVQRKKC-----QKG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING STRAIN-Bristol N2;
                                                SIMILARITY.
                                                                                                                                                                                                                                                                                                                  23; Mismatches
                                        SIMILARITY
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                                                                                                                                                                                                                         SIMILARITY
 9.7%;
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Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                   Best Local Similarity 24.8% Matches 54; Conservative
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H. (BY SIMILARITY).  BM (BY SIMILARITY).  BM (BY SIMILARITY).  FIIAL).  CPOTENTIAL).  CPOTENTIAL).	/FILE-NSP 006416. VEESARS.FPDLTSGWILG.CDECNGGCTESSSATSCFAYKH L-> LCFWIEDSOPTECVCLRVCERGVIINFQIEKLKKST KCLIFS (in isoform E). /FILE-NSP_005417. VETIG-NSP_015417. VEESARS.FPDLTSGWILSCDECNGGCTESSSATSCFAYKH LTGTLTRNKGGSGFKCVQKCDDTYYLLGGNKCKM -> GDEVV ERIRHWEVTLEESSHWIWEHAREHKSLQELNSSSRTHSFL SFFIKFQEIFLILLVCIFDAIHRQFAV (in isoform B).	fridasing (in isoform A).  /FTId=VSP_005419.  Missing (in isoform B).  /FTId=VSP_005420.  Missing (in isoform B).  /FTId=VSP_005421.  GENLVQAKCIWRKDLCGDGYYINAVGKCDLCDSSCETCTAP  GENLVQAKCIWRKDLCGDGYYINAVGKCDLCDSSCETCTAP  GENLVQAKCIWRKDLCGDGYYINAVGKCDLCDSCETCTAP  GENLVQAKCIWRKDLCGDGYYINAVGKCDLCDSCCTCTAP  FFIGHAVSP_005421.  KDYCNLKLVDLDFFIFSLLF (in isoform C).	CC). CRC64; Length 943; Indels 50; Gaps 11;
4 H H H 4	/FTIGLWSP 005416. VEESARSFPDITSGWILSCDE L -> LCFNPENSQPTECVCLIR L AS LCFNPENSQPTECVCLIR KCLIFS (in isoform 8). /FTIGLWSP 005417. VEESARSPPDITSGWILSCDE LTQTLANKGGGFFCVVQKCDT ERIRHWEVTLEESSHWNWEHA YSPTKCPPILLIVCIFDALH B).	Missing (in isoform A).  /FIId=VSP_005419.  /FIId=VSP_005419.  Missing (in isoform B). /FIId=VSP_005420.  Missing (in isoform B). /FIId=VSP_005421.  ESNLVQAKCIWRKDLGGDGYXINAVGKCDLCDS GPMSCRKC -> ARNVPECAXNNESGROTIVEN KDYCNLKLVDLDFFIPSILF (in isoform /FIId=VSP_005422.	Missing (In isoform //FTId=vSP 005423. A - R (IN REF. 2). S -> R (IN REF. 2). 46 MW; 401E009E6C46AD7E6; Score 145; DB 1; 6%; Pred. No. 0.0031; 6%; Mismatches 77;
11 9 2 2 4 4 8 6 8 1 4 4 6 6 8 8 6 7 8 6 7 6 7 6 7 6 7 6 7 6 7 6	730	943 943 828 828	o. ~w. Ø
21 2012 2013 4114 4117 7113 658	658 658	671 700 731 780	C 829 T 153 T 346 B 943 AA; h Similarity 51; Conser
PROPEP CHAIN ACT_SITE ACT_SITE ACT_SITE TRANSKEM DOMAIN DOMAIN CARBOHYD VARSPLIC	VARSPLIC	VARSPLIC VARSPLIC VARSPLIC VARSPLIC	VARSPLIC 829 CONFLICT 153 CONFLICT 346 SEQUENCE 943 AA; Query Match Best Local Similarity Matches 51; Conserv
			FFFFS Onz

Search completed: June 29, 2004, 17:00:16 Job time : 12.2828 secs

035171 mus musculu Q8cfz2 mus musculu Q62030 mus musculu Q86pq3 cryptospori Q96ep4 homo sapien O18003 caenorhabdi Q90018 giardia lam O42114 brachydanio O76822 branchiosto

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mus musculu

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042113 brachydanio 09924 xenopus lae 076510 cryptospori 086xx4 homo sapien 099244 rattus sp. 094862 homo sapien 094862 homo sapien 094862 homo sapien 023832 cryptospori 09bi05 eimeria ten 0991x9 bos taurus 0991x9 bos taurus 080xc9 mus musculu 080xc9 mus musculu

299q41 giardia lam

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SEGUENCE FROM N.A.
Mao Y., Xie Y., Zhou Z., Zhao W., Zhao S., Wang W., Huang Y., Wang S.,
Tang R., Chen X., Wu C.,
Submitted (MAR-2000) to the EWBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 HLRLISWLFIILNFWEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | TISSUE=Placenta; | SEQUENCE FROM N.A. | TISSUE=Placenta; | Straubserg R.; | Submitted (FRB-2002) to the EMBL/GenBank/DDBJ databaseg. | EMBL; AP251057; AAK34947.1; - RMBL; BAC51057; AAK34947.1; - RMBL; BAC51057; AAK34947.1; - RMBL; ROO052376; ARSDZ R.; | STROUBSUE RED RECEPTORY IPRO00684; TSP1. | STRAT; SM00261; FU; 2. | STRAT; SM00261; FU; 2. | STRAT; SM00261; FU; 2. | STRAT; SM00209; TSP1; 1. | STRAT; SM00209; TSP1; 1. | STRAT; SM002109; TSP1; 1. | STRA
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Q9GQ45
Q80T14
Q9W770
Q924Y6
Q9HCB6
Q9HCB6
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09B105
09GLX9
099KR2
08K2Q8
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Q96EP4
O18003
Q9U018
O42114
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Q9PVZ4
O76510
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2003 (TrEMBLrel. 25,
Thrombospondin.
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Homo sapiens (Human)
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Matches 271;
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Q9BXY4
SO DE RESERVACIONES DE LA PRESENTACION DE LA PRESEN
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Q9csD2 mus masculu
Q9csD2 mus musculu
Q8by23 mus musculu
Q81312 mus musculu
Q8n715 homo sapien
Q8n716 homo sapien
Q8n6x6 homo sapien
Q9n6x6 homo sapien
Q7fpx3 mus musculu
Q8n6x7 aus musculu
Q8n6x7 aus musculu
Q8n6x7 aus musculu
Q8n6x1 aus musculu
Q8ax10 rana escule
Q964Q2 entamoeba h
Q8szsz drosophia
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1516
1 MGHLRLISWLPIILNPMEYI......QQKKRKVQDKQKSVSYVSTVH 273
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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sp_vertebrate:*
sp_unclassified:*
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sp_archeap:*
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Gapop 10.0 , Gapext 0.5
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Last sequence update) Last annotation update)

Created)

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Gaps

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Length 272;

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243 KEI PEORENKOOOKKRKVODKOKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKFDNKGESKRAIPDSKSLESS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFALERIGAKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNPCTKCKSGFYLH 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 PFALERIGARQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNPCTKCKSGFYLH 121
                                                                                                                                                                     123 LGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQ 182
                                                                                                                                                                                              122 LGKCLDNCPEGLEANNHTWECVSIVHCEVSEWNPWSPCTKKGKTGGFKRGTETRVREIIQ 181
                                                                                                                                                                                                                                                             HPSAKGNLCPPTNETTRKCTVQRKKCQKGBRGKKGRBRKRKKPNKGBSKBAIPDSKSLBSS 242
                                                                         122
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HPSAKGNI,CPPTNETRKCTVQRKKCQKGRRKKKRRRKRKPNKGESKBAIPDSKSLESS
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                                                                         PPALER I CARKO I GVCLSS CPSGYYGTRYPD INKCTRCKADCDTCFNKNPCTKCKSGFYLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Embryo;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Takahashi-Pujii A., Hara H.,
Tanase T., Nomura Y., Togiya S., Komai P., Hara R., Takeuchi K.,
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Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AK027346; BAB55051.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Kominidae, Komo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 292 Aa; 33243 MW; 01E2774AC3D4A6F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ14440
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                          243 KEIPEGRENKQQQKKRKVQDKQKSVSVSTVH 273
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InterPro; IPR009030; Grow Fac_recep.
InterPro; IPR000884; TSP1.
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SMART; SM00261; FU; 2.
SMART; SM00209; TSP1; 1.
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Carraine-Cs7BL/64; Tissus-Embryo;

MEDLINE-21085660; PubMed=11217851;

MEDLINE-21085660; PubMed=11217851;

Marawa J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 AA; 24304 MW; 0DCF938B9FB3FBF7 CRC64;
                                                                                                                                                                                                                                                                                             01-07N-2001 (TrEMBLrel. 17, Created)
01-07N-2001 (TrEMBLrel. 17, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
2810459404Rik protein (Fragment).
THSD2 OR 2810459404RIK.
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InterPro; IPR006212; Purin repeat.
InterPro; IPR006303; Grow_fac_recep.
InterPro; IPR00084; TSP1.
Pfam; PF00090; tsp_1; 1.
SMART; SM0021; F07; 2.
SWART; SW00209; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
242 KEIPEGRENKQQKGRKVQDKQKS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 93.13 tes 201; Conservative
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Gaps

24;

Length 265;

63

RESULT 4 QBBVW2

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Consider A., Takabashi-Pujii A., Tanase T., Imose N., Takeuchi K., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yanamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yanashita H., Marsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kamehori K., Sugiyama A., Kawakami B., Suzuki Y., Sugiyama A., Kawakami B., Suzuki Y., Wagano G., Nagahari K., Masuho Y., Nagai K., Isogai T.; Submitted (JUL.2002) to the EWEL/GenBank/DDBJ databases.

EMBL; AKO98225; BACO526:1; Surin repeat.

InterPro; IPR00084; TSP1.

InterPro; IPR000829; TSP1; 1.

SWART; SM0026; FU; 2.

SWART; SM0029; TSP1; 1.

W Hypothetical proctein.

W Hypothetical proctein.
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                                                                                                                                                                                                                                                                                                                        6 LISWLPIILNPMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRLFPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 KCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGPKRGTETRVREIIQHP
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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48.1%; Pred. No. 1.5e-49;
ive 36; Mismatches 69; Indels 15.
InterPro; IPR006212; Furin repeat.
InterPro; IPR009030; Grow Fac_recep.
InterPro; IPR00084; TSP1.
Ffam; PF000100; tsp. 1; 1.
SWART; SM00261; FU; 2.
SWART; SM00209; TSP1; 1.
PR0SITE; PS0092; TSP1; 1.
PR0SITE; PS0092; TSP1; 1.
SRQUENCE 265 AA; 29331 MW; FFBB8964743F5963 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                  42.5%; Score 644; DB 11;
46.5%; Pred. No. 4.1e-51;
ive 36; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236
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Homo sapiens (Human).
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                                                                                                                                                                                                                                                    Matches 119; Conservative
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Matches 111; Conservative
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                                                                                                                                                                                                                            Best Local Similarity
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Q8N7L5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 PFVLERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKVDCDTCFNQNPCTKCKSGFYLH 121
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                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CS7BL/6J; TISSUR=Skin; MEDLINE=22354683; PubWed=12466851; The PANTOM CONSOrtium: The PANTOM Consortium: the RIKEN Genome Exploration Research Group Phase I & II Team; Ahalysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 HIRLISCFFIILNFMEXIGSQNASRGRRQRRWHPNVSQCQGGCATCSDYNGCLSCKPRL
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"R-spondin, a novel thrombospondin type I domain gene, expressed in the dorsal neural tube.";
Submitted (MIG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB016/68; BAA75640.1; -...
MGD; MGI:2183426; Rspondin.
                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 70.2%; Score 1064; DB 11; Length 224; Best Local Similarity 84.6%; Pred. No. 1e-89; Matches 187; Conservative 9; Mismatches 25; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00261; FU; 2. _ _ SQUENCE 224 AA; 25398 WW; BC13B083497CFBB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 HPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKK 223
                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Thrombospondin type 1 domain.
RSPONDIN OR R-SPONDIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265 A.A.
                                                                                            224 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60,770 full length cDNAs.";
Nature 420,563-573 (2002).
EMBL, AKO76308; BAC36296.1;
InterPro; IPR006212; Purin repeat.
InterPro; IPR009930; Grow_fac_recep.
                                                                                                                                         Created)
                                                                                            PRT;
                                                                                                                                       23,
23,
                                                                                            PRELIMINARY;
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                                                                                                                                                            01-MAR-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                       (TrEMBLrel.
                                                                                                                                                                                                                                 THSD2 OR 2810459H04RIK.
                                                                                                                                                                                                       Thrombospondin homolog
                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE PROM N.A.
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                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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                                                                                                                                       01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123
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                                                                                       Q8BVW2
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STRAIN=C57BL/61; TISSUE=Bye, and Hippocampus;

X MEDLINE=22354683; pubMed=12466851;
X TARAIN=254683; pubMed=12466851;
X TARAIN=254683; pubMed=12466851;
X The FANYOM Consortium,
X The FANYOM Consortium,
X The RANYOM Consortium,
X THE AKO4981; BAC39893.1; -.
X EMBL; AKO49891; BAC39893.1; -.
X RANY; SMO0261; FU; 2.
X INTERPRO; IPRO009894; TSP1.
X SMARY; SMO0261; FU; 2.
X SMARY; SMO0261; FU; 3.
X SMARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 MYKCIKCKIEHCEACPSHVPCTKCKGGLYLHKGRCYPACPEGSSAANGINGCSSPAQCBV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTBTRVREIIQHP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAKGNLCPPTNETRKCTVQRKKCQKGERGKKRKRKKPNKGESKRAIPDSKSLESSKR 244
                                                                                                                                                                                                  152 SEWNPWSPCTKKGKTCGFKRGTETRVREIIQHPSAKGNLCPPTNETRKCTVQRKKKCQKGE 211
                                                                                                                                                                                                                               LERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKAD-CDTCFNKNFCTKCKSGFYLHLG 124
                                                                                                  93 INKCTKCKAD-CDICFNKNPCTKCKSGPYLALGKCLDNCPEGLBANNHTMECVSIVHCEV 151
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6 LISWLPIILNPWEYIGSQNASRGRRQRRMHPNVSQCQGGCATCSDYNGCLSCKPRLFPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                     212 RGKKGRERKRKKPNKG----ESKEAIPDSKSLESSKEIPEQRENKQQQKKR 258
                                                                                                                                                                                                                                                                                                                                    Query Watch
38.0%; Score 576.5; DB 11; Length 243;
Best Local Similarity 45.0%; Pred. No. 5.9e-45;
Matches 108; Conservative 39; Mismatches 78; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 AA
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01-MAR-2003 (TrEMBLrel. 23, Last sequence
10-CT-2003 (TrEMBLrel. 25, Last annotatio
Hypothetical thrombospondin type I repeat.
2610028F08RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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RESULT 8

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89 RYPDINKCTKCKADCDTCPNKNPCTKCKSGPYLHLGKCLDNCPEGLEANNHTMECVSIVH 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 RRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRLFFALERIGMKQIGVCLSSCPSGYYGT
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                                                                                                                                                                                  Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                           01-KAY-2000 (TrEWBLrel. 13, Created)
01-CCT-2001 (TrEWBLrel. 18, Last sequence update)
01-CCT-2003 (TrEWBLrel. 25, Last annotation update)
01-CCT-2003 (TrEWBLrel. 25, Last annotation update)
01-CCT-2003 (TrEWBLrel. 25, Last annotation update)
050424P16.3 (Novel protein 8-spondin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 224;
                                                                                                                                                                                                                                                                                                      Blakey S.; Caber S. Blakey S.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
REMBL, ALOS0325; Caber783.3; -
REMBL, ALOS0325; Caber782.
InterPro; IPR066212; Purin repeat.
InterPro; IPR060303; Grow_Fac_recep.
InterPro; IPR000884; TSP1.
R SWART; SW00209; TSP1, 1.
R PROSITE; PS500229; TSP1, 1.
R PROSITE; PS500229; TSP1, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
31.1%; Score 472; DB 4; Length 22
Best Local Similarity 43.3%; Pred. No. 2.1e-35;
Matches 87; Conservative 36; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC027938; AAH27938.1; -.
InterPro; IPR065212; Furin repeat.
InterPro; IPR090303; Grow Fac_recep.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 224 AA; 25042 MW; 97D26AD34CDBFB12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
224 AA
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01-CCT-2002 (TrEMBLrel. 22, Created)
01-CCT-2002 (TrEMBLrel. 22, Last seq
01-CCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 PGERSPGQXKGRKDRRPRKDR 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00261; FU; 1.
SMART; SM00209; TSP1; 1.
PROSITE; PS50092; TSP1; 1
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similar to putative. Homo sapiens (Human)
                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. TISSUE-Lung;
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63 LRREGMROYGECLHSCPSGYYGHRAPDMNRCARCRIENCDSCFSKDFCTKCKVGFYLHRG 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 RRORRMHPNVSQCCQGCCATCSDYNGCLSCKPRLFFALERIGMKQIGVCLSSCPSGYYGT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AKO20904; BAC25643.1; -.
MGD; MGI:1924467; A930029K19Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spodoptera frugiperda (Fall armyworm).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae; Amphipyrinae; Spodoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 RYPDINKCTKCKADCDTCFNKNPCTKCKSGPYLHLGKCLDNCPEG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00261; FU; 2. SEQUENCE 138 AA; 15172 MW; FEFD7D949279D5DD CRC64;
                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                      125 KCLDNCPEGLEANNHTMECVSIVHCEVSEWN 155
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InterPro; IPR009030; Grow_fac_recep.
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                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/61; TISSUE=Retina;
MEDLINB=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                   (TrEMBLrel. 23,
(TrEMBLrel. 23,
(TrEMBLrel. 25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                         (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                           A930029K19RIK.
Mus musculus (
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01-MAR-2003 (
01-OCT-2003 (
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Q26489;
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WEDLINE-2138L/63; TISSUE-Egg;

MEDLINE-2138L/63; TISSUE-Egg;

MEDLINE-2138L/63; TISSUE-Egg;

RIJANA-C57BL/64; TISSUE-Egg;

RAMA-C57BL/64; TISSUE-Egg;

RAMA-C57BL/64;

RA
                                                                                                             'n
                                                                                                                                                           71 MKQIGVCLSSCPSGYYGTRYPDINKCTKCKAD-CDTCPNKNPCTKCKSGPYLHLGKCLDN 129
                                                                                                                                                                                                                                                                130 CPEGLEANNHIMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQHPSAKGN 189
                                                                                                                                                                                                                                                                                                               61 CPDGPAPLEETWECVE - GCEVGHWSEWGTCSRNNRTCGPKWGLETRTRQIVKKPVKDTI 118
                                                                                                                                                                                    66 LERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKAD-CDTCFNKNFCTKCKSGFYLHLG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 LFSFALIILNCMDYSQCQ-GNRWRRNKRA-SYVSNPICKGCLSCSKDNGCSRCQQKLPFF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 LISWLPIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRLPFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                       13; Gaps
                                                                                                                                                                                                                                                                                                                                                                     190 LCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGESKEAIPDSKSLESSKE 244
                                                                                                                                                                                                                                                                                                                                                                                                   119 PCPTIABSRRCKMTPRHCPGGKRTPKAKEKRNKKKKR------KLIERAQE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŝ
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                                                      Length 176;
                                                   Query Match 30.3%; Score 459.5; DB 4; Length Best Local Similarity 45.1%; Pred. No. 2.3e-34; Matches 79; Conservative 30; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
  20409 MW; OF83CCE1B2F8CA85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 AA; 17658 MW; B74713789B2853B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Egg;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; BC052844; AAH52844.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2610028F08Rik protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 79; Conservat
  176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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  SEQUENCE
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Q7TPX3 RESULT 10 Q7TPX3

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632 GPCDARCSDV-GCDGPGPHHCNDCLHFYYK--AKNNTRICVSDCPLGYYPA---DKKRCK 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 KCKADCDTCP--NKNPCTKCKSGPYLH--LGKCLDNCPEGLEANNHTMECVSIVHCEVSE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 GGC-ATCSDYNGC----LSCKPRLFPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 WNPWSPCTKKGKTCGPKRGTETRVREIIQHP-SAKGNLCPPTNET-RKCTVQRKKCQ 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=HM:1MSS;
MEDLINE=21391855; PubMed=11500468;
MEDLINE=21391855; PubMed=11500468;
Cheng X.J., Hughes M.A., Rhuston C.D., Loftus B., Gilchrist C.A.,
Lockhart L.A., Ghosh S., Miller-Sims V., Mann B.J., Petri W.A. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tachibana H.;
Tachibana H.;
Intermediate Subunit of the Gal/GalNAc Lectin of Entamoeba
histolytica Is a Member of a Gene Family Containing Multiple CXXC
Sequence Motifs. F.;
Infect. Immun. 69:5892-5898 (2001).
EMBL; AR337950; AAK92361.1; -
GO; GO:0005529; Fasugar binding; IRA.
GO; GO:0007157; P:heterophilic cell adhesion; IRA.
InterPro; IPR006209; EGF_like.
InterPro; IPR009030; Grow fac_recep.
FROSITE; PS01186; EGF_2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.8%; Score 179.5; DB 13; Length 913; 29.4%; Pred. No. 5.9e-08; tive 22; Mismatches 66; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
11.7%; Score 177; DB 5; Length 1101;
Best Local Similarity 26.6%; Pred. No. 1.2e-07;
Matches 55; Conservative 22; Mismatches 80; Indele 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 1101 AA; 119512 MW; C8B6F5CBDB656AEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               913 AA; 101864 MW; 6C9020632C47D9BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DCT-2003 (TrEMBLrel. 25, Last annotation update)
Gal/GalNAc lectin Igl1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1101 AA
                                         InterPro; IRROGGIO; ISGR.
InterPro; IPROGGIO; IEGF.
InterPro; IPROGGIO; Peptidase_SB.
InterPro; IPROGGIO; Peptidase_SB.
InterPro; IPROGGIO; Peptidase_SB.
InterPro; IPROGGIO; Protease_Inhib.
Pfam; PPOGGIO; Perinalike; 1.
Pfam; PPOGGIO; Perinalike; 1.
Pfam; PPOGGIO; Perinalike; 1.
Progrip : PROGGIO; Perinalike; 1.
PROGGIT; PROGGIO; PROG
Purin repeat.
Grow_fac_recep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Entamoeba histolytica.
Eukaryota, Entamoebidae, Entamoeba.
NCBI_TaxID=5759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 29.4*
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q964D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
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Gangnon F., Jegou S., Vallarino M., Vieau D., Vaudry H.;
TWO lecular characterization of the cDNA and localization of the mRNA encoding the probormone convertage PC5-A in the Buropean green frog.";
J. Comp. Neurol. 0:0-0(2002).

BYMEL, AV131292, AANN10146:1, -.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:000524; F:ATP binding; IEA.

GO; GO:000523; F:Peptidase activity; IEA.

GO; GO:0004289; F:subtilase activity; IEA.

GO; GO:0004289; F:subtilase activity; IEA.

GO; GO:000618; P:peptidase activity; IEA.

GO; GO:000618; P:electron transport; ED.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

GO; GO:000648; P:protein amino acid phosphorylation; IEA.

GO; GO:000648; P:protein amino acid phosphorylation; IEA.

GO; GO:000169; P:transmembrane receptor protein tyrosine kin. ..; IEA.

InterPro; IPR006211; Furin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 844 CAKCHESCDICQGPGETQCVTCHPSTYALDGRCVTSCPPAYYADKKRKEC---MRCPVG- 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 WNPWSPCTKKGKTCGFKRGTETRVREIIQHPSAKGNICPP---TWETRKC-TVQRKKCQK 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 SVCRPCAAHCATCSBRADGCTSCEHHL-----VLHDGTCMASCPPSHYBT---BDDM 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96 CTKCKADCDTCP--NKNPCTKCKSGPYLHLGKCLDNCPEGLEANNHTMECVSIVHCEVSE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---CSTCT------SAPCLSCEPKWBLNKGKCMPVGSDKCSA 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 NVSQGCQGCCATCSD-YNGCLSCKPRLPFALERIGMKQIGVCLSSCPSGYYGTRYPDINK 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serine procease PC5-A.
Serine procease PC5-A.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana, VCBI_TaxID=8401,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 GERGKKGRERKRKKPNK-----GESKE---AIPDSKSLESSKEIPE 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R GO; GO:000823; F:Peptidase activity; IEA.

R GO; GO:000823; F:Peptidase activity; IEA.

R GO; GO:0004289; F:Subtilase activity; IEA.

R InterPro; IPR00512; Furin repeat.

InterPro; IPR00512; Furin repeat.

InterPro; IPR00512; Peptidase_SB.

InterPro; IPR00510; Grow_Fac_recep.

InterPro; IPR00510; Peptidase_SB.

InterPro; IPR00510; Peptidase_SB.

R InterPro; IPR00510; Protease Inhib.

R Pfam; PR001082; Peptidase_SB; I.

R Pfam; PR01483; Proprofein; I.

R PRINTS; PR00723; SUBTILISIN.

R PROSITE; PS00113; SUBTILIASE ASP; I.

R PROSITE; PS00113; SUBTILIASE HIS; I.

R PROSITE; PS00139; SUBTILIASE HIS; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.7%; Score 192; DB 5; Length 1299; 27.8%; Pred. No. 6e-09; vative 26; Mismatches 78; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 27.84
Matches 63; Conservative
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Gaps

20;

11;

37; Gaps

---PCORGCKTC----TSNGVCS 873

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120 YLHLGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTXXGKTCGFKRGTETRV-R 178
784 LVMHEHK------CYSACPLDTYET---EDNKCAFCHSTCATCNGPTDQDCITCRSSR 832
                                                                                                                                           179 BIIOHPSAKGNLCPPINBTRKCTVORKK-COKGE
                                                                                                                                                                                                                 Search completed: June 29, 2004, 17:02:12
Job time : 37.7876 secs
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833 YAWQNKCLISCPDGFYADKKRLBCM-
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                    90 YPDINKCTKCKADCDTCFNKNPCTK------CKSGFYLHLGKCLDNCPEGLEA 136
                                                                                                                                                                                 885 TWHCSECSSAARCTVCESDTYKVISGNGCNSCVDGF-----YFDBIKGTCIPC 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 NNHTMECVSIVHCEVSEMNPWSPCTKKG-KTC--GFKRGTETRVREIIQHPSAKGNLCPP 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
GGCATCSD---YNGCL---SC---KPRLFPALE----RIGMKQIGVCLSSCPSGYYGTR 89
                                                                                                    3 HIRLISWIFILLNFWEYIGSQNASRGRRORRMHPNVSQGCQGGCATCSDY-WGCLSCKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Berkeley;
Stapleton M., Broktein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Friee E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.6%; Score 176.5; DB 5; Length 1376; 28.0%; Pred. No. 1.7e-07; Indels 53; Live 24; Mismatches 77; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LD30182p.
FUR2 OR CG4235 OR CG18734.
Drosophila melanogaeter (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukeryota; Endopterrygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
-!- SIMILARITY: CONTAINS 1 HCMO B/P DOWAIN.
EMBL, ANOTOSS3, AALAGO24-1; --
FYDASS; FEGNOGO4598; Puz.
GO; GO:0004276; F:furin activity; IDA.
InterPro; IPR0004598; Cytc.Heme_BS.
InterPro; IPR000612; Furin repeat.
InterPro; IPR000613; Furin repeat.
InterPro; IPR000613; Furin repeat.
InterPro; IPR000613; Peptidase_S8.
InterPro; IPR000613; Peptidase_S8.
InterPro; IPR000613; Peptidase_S8.
InterPro; IPR000613; Peptidase_S8.
InterPro; IPR00181; Peptidase_S8.
INTERPROSITE; PS0019; CYTOCHROME C; 3.
INTERPROSITE; PS00119; SUBTILASE_ASP; 1.
IPROSITE; PS00118; SUBTILASE_ASP; 1.
IPROSITE; PS00118; SUBTILASE_ASP; 1.
IPROSITE; PS00118; SUBTILASE_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protease, Serine protease.
1376 AA; 149716 MW; B6704BA89A3A88FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                            PRT; 1376 AA.
                                                                                                                                                                                                                                    194 TNETRKCTVQRKKCOKGERGKKGRERK 220
                                                                                                                                                                                                                                                                           TSPCTKCVGVKCCEEORTGCNSRKKK 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60; Conservative
                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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Matches 60
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05-APR-2000; 2000US-00543774.
28-JUN-2000; 2000US-0215733P.
09-JAN-2001; 2001US-00757562.
05-PEB-2001; 2001US-0266614P.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                  1586107 segs, 282547505 residues
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                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                 first 45 summaries
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AAW85607
AAB13170
ABP61846
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ABO44431
AAB99220
AAM78328
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AAE13150
ABR62112
ABO44432
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AB044434
AAE13163
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AB044417
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ABB11374
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                                                   June 29, 2004, 16:54:09
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Gapop 10.0 , Gapext 0.5
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geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
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Maximum DB seq length: 200000000
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Match Length
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1315.5
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						RESULT 1
	ALIGNMENTS					
Aael3155 Human SCR	AAB13155	4	46	17.4	267	45
Novel	ADB76146	1	234	29.3	450	44
	ABR62102	9	229	34.6	531.5	43
Abr62107 Secreted	ABR62107	9	222	34.9	536	42
Abr62101 Secreted	ABR62101	9	250	36.8	565	41
Aae36166 Mouse SCR	AAB36166	9	243	36.8	565.5	40
Abr62106 Secreted	ABR62106	9	243	37.1	569.5	39
Abg76508 DNA encod	ABG76508	'n	243	37.1	569.5	38
Aae37115 Human sec	AAB37115	9	243	37.2	571.5	37
Abo44426 Mouse thr	AB044426	9	229	41.0	629	36
_	AAE13162	4	229	41.0	629	35
Abr62113 Mouse thr	ABR62113	ø	265	41.2	632	34
۰	ABR62110	9	243	41.7	640.5	33
_	ADE07919	~	263	42.2	648	32
	ABR58489	9	263	42.2	648	31
Abr62115 Secreted	ABR62115	9	263	42.2	648	30
	ABR62108	9	263	42.2	648	29
	AB044415	9	160	49.4	759	28
Aael3149 Human ste	AAB13149	4	160	49.4	759	27
Human	AAM79312	4	160	49.4	759	56

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Mouse, stem cell growth factor-like protein, antiinflammatory; nootropic; neuroprotective; vulnerary; cytostatic; anticonvulsant; immunostimulant; vasotropic; virucide; dermatological; tranquilliser; cerebroprotective; obsecpathic; immunodeficiency syndrome; chronic granulomatous disease; duplicated immunodeficiency syndrome; wiskott-Aldrich syndrome; AIDS; acquired immunodeficiency syndrome; agammaglobulinaemia; thalassaemia; daucher's disease; lysosomal storage disease; mucopolysaccharidosis; parkinson's disease; Alzheimer's disease; thrombocytopaenia; SCID; severe combined immunodeficiency; immune disorder; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; autoimmune pulmonary inflammation; cancer; tumour; gene therapy; SCR-1; supporting factor for the proliferation of stem cell.
                                                                                                                                                                                                                                                                                    Mouse stem cell growth factor-like protein.
AAB13167 standard; protein; 279 AA.
                                                                                                                                                                                      (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                      28-JAN-2002
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1. .21 /label= Signal_peptide 22. .279 /note= "Mouse mature stem cell growth factor-like protein" Location/Qualifiers

#0200177169-A2

05-APR-2001; 2001WO-US011208

HYSEQ INC. KIRIN BEER KK.

Drmanac RT; ບັ Liu Tang TY, Labat I, Tillinghast JS, Sinku A,

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The patent discloses novel stem cell growth factor-like proteins and polymucleotides encoding them. Proteins of the invention are also known as supporting factor for the proliferation of stem cells (SCR-1). Stem cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell, encoded the proliferation or survival of a stem cell, encoded the proliferation or survival of a stem cell, encoded the proposition of a stem cell, pluripotent cell, hasmatopoietic progenitor cell, pluripotent cell, hasmatopoietic progenitor cell, pluripotent cell or totipotent cell. The hasmatopoietic progenitor cell, pluripotent cell or totipotent cell. The hasmatopoietic progenitor cell cultured using stem cell growth factor-like proteins can replace as agraft for the bone marrow cramplantation or cord blood transplantation for treating a variety of diseases such as immunodeficiency syndrome, chronic granulomatous diseases, duplicated immunodeficiency syndrome, agammaglobulinaemia, hasman, hasmania, daucher, sidesease, lysosomal storage cuch as sickle cell anaemia due to enzyme defect, congenital anaemia cuch as sickle cell anaemia, daucher, adisease, lysosomal storage diseases such as mucopolysaccharidosis, adrenal white matter degeneration, a variety of cancer and tumours. Proteins of the invention are useful for treating diseases such as parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, thrombocytopaenia, immune deficiency syndromes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SCID)) and autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, and autoimmune pulmonary inflammation. Sequences of the invention are also useful in gene therapy. The present sequence is stem cell growth factor-like protein from mouse
                                                                                                                                               Novel stem cell growth factor like polypeptides and polynucleotides for identifying modulators useful for treating diseases such as Alzhelmer's
                                                                                                                                                                                                                 disease, cancer, rheumatoid arthritis, osteoporosis
Mize NK, Nishikawa M;
                                                                                                                                                                                                                                                                         Claim 28; Page 223-224; 232pp; English.
   Stache-Crain B, Dickson M,
                                                              2001-657166/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 279 AA;
                                                                                          N-PSDB; AAD21727
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61 LPFVLERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKVDCDTCFNKNFCTKCKSGFYL 120
                                                                                                                                                                                                                                                                181 QHPSAKGKGNLCPPTSETRTCIVQRKKCSKGERGKKGRERKRKTANKEERKETSSSSDSK 240
                                                                                                                                                                                                                                             HLGKCLDSCPEGLEANNHTMECVSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDIL 180
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                                                                                                                                                             LFFVLERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKVDCDTCFNKNFCTKCKSGFYL
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                                         Gaps
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100.0%; Score 1535; DB 4; Length 279; 100.0%; Pred. No. 6.2e-109; ive 0; Mismatches 0; Indels 0
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Query Match
Best Local Similarity 100.
Matches 279; Conservative
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Mouse stem cell growth factor-like protein.
                           ABO44431 standard; protein; 279
                                                                              (first entry)
                                                      AB044431;
RESULT 2
AB044431
ID AB04
XX
AC AB04
XX
XX
DT 30-S
XX
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Stem cell growth factor-like protein, antianemic; anti-HIV; SCR-1; immunostimulant; vulnerary; haematopoietic stem cell; gene therapy; supporting factor for proliferation of stem cells; wound healing; haematopoietic progenitor cell; stromal cell; AIDS; thalassaemia; chronic aransplantation; cord blood transplantation; chronic granulomatous disease; duplicated immunodeficiency syndrome; agammaglobulinaemia; Miskott-Aldrich syndrome; haemolytic anaemia; congenital anaemia; sicklaemia; dauchar's disease; morphogenesis; epithelial cell growth; ovarian follicle development; nerve cell growth; cartilage remodeling; bone growth; immunosuppression; mouse. .21
 /label= Signal_peptide Location/Qualifiers Aus musculus. Peptide

22. .279
/note= "Mature stem cell growth factor-like protein. This protein is specifically claimed in claim 9" ΰ Mize N, Nishikawa M, Drmanac RT, 28-JUN-2000; 2000US-0215733P. 05-FEB-2001; 2001US-0266614P. 05-APR-2001; 2001US-0282397P. 28-JUN-2001; 2001US-00894912 WPI; 2003-625403/59. DRMANAC R T. NISHIKAWA M. CHAO C. Labat I, TANG Y T. N-PSDB; ACH04327 US2003044792-A1. LABAT I MIZE N. 06-MAR-2003 Tang YT, (NISH/) Protein TANG/) (DRMA/) (MIZE/) (LABA/) 

The invention relates to an isolated stem cell growth factor-like polypeptide (referred as supporting factor for proliferation of stem cells (SCR-1) from mouse or human, or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity. Also included are an isolated polymucleotide encoding CG SCR-1 (or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity, or the complement of the polymucleotide, an (expression) vector comprising the SCR-1 polymucleotide, a host cell genetically engineered to contain the SCR-1 polymucleotide in operative association with a regulatory sequence that controls expression of the polymucleotide in the host cell, or expression product of the SCR-1 polymucleotide (the polypeptide having an expression product of the SCR-1 polymucleotide (the polypeptide having an equivity to support proliferation or survival of haematopoietic stem cell, with a proviso that C-terminal as sequence does not comprise the as sequence appearing as ABO44433), an isolated sorn and conservity and isolated sorn propertive ass from ABO44430, an isolated polypeptide

I lacking any 10 consecutive ass from ABO44430, an isolated polypeptide Novel isolated polypeptide having stem cell growth factor activity, useful for promoting wound healing, and as a medicine to proliferate or support human hematopoietic stem cells or human hematopoietic progenitor cells. Claim 23; Page 80; 96pp; English.

with stem cell growth factor activity having at least an as sequence appearing as ABO44428 and ABO4429, a culture medium comprising the SCR-1 polypeptide to maintain survival of or promote proliferation of a stem cell or germ cell, an anti-SCR 1 antibody, a nucleic acid array comprising the SCR-1 polymucleotide or a unique segment of the SCR-1 polymucleotide, a stromal cell genetically

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engineered to express the SCR-1 polypeptide to support proliferation or survival of a stem cell or germ cell and an implant comprising a cell genetically engineered to express the SCR-1 polypeptide to support proliferation or survival of a stem cell. The SCR-1 polypeptide and for maintaining survival of or promoting proliferation of a stem cell, a germ cell, a demanicabiling survival of or promoting proliferation of a stem cell. The SCR-1 polypeptide is useful for promoting proliferation of a stem cell. The SCR-1 polypeptide is useful for promoting wound castem cell. The SCR-1 polypeptide is useful for promoting wound castem cell. The SCR-1 polypeptide is useful for promoting wound castem cell. The SCR-1 polypeptide is useful for promoting wound caste for the conventional bone marrow transplantation or cord blood graft for the conventional bone marrow transplantation or cord blood caste for the conventional bone marrow transplantation or cord blood diseases, duplicated immunodeficiency syndrome, agammaglobulinaemia, diseases, duplicated immunodeficiency syndrome, agammaglobulinaemia, due to enzyme defect, congenital anaemia such as sicklaemia, Gaucher's disease etc. the SCR-1 polypeptide is useful for cell growth and regulation, ovarian follicle development, promoting nerve cell growth, austaining neuronal populations, cartilage remodeling, bone propersia
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malignant tumour; haemopathy; HIV infection; immunological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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inflammation disease.
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The present sequence is the protein sequence for human thrombospondin-30. Thrombospondin-30 protein and coding sequence are useful in the diagnosis and treatment of malignant tumour. haemopathy, HIV infection, immunological diseases and various inflammation diseases. In addition thrombospondin-30 protein may be used for screening mimics, agonists, antagonists or inhibitors, or for use in peptide fingerprinting identification. The thrombospondin-30 coding sequence may be used as primers for nucleic acid amplification reaction or as probes for hybridisation reaction, or in producing gene chips or microarrays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 HLGKCLDNCPEGLEANNHTWECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LFFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIGKCLDSCPEGLEANNHTMECVSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 QHPSAKGKGNLCPPTSETRTCIVQRKKCSKGBRGKKGRBRKRKKLNKERKRTSSSSDSK 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                             Human thrombospondin-30 and polynucleotide is useful in diagnosis and
treatment of, e.g., malignant tumor, hemopathy, HIV infection,
immunological diseases and various inflammatory diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MHIRLISWIPTILWFWEYIGSQNASRGRRQRRWFPNVSQGCQGGCATCSDYNGCLSCKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LPPVLBRIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKVDCDTCFNKNPCTKCKSGFYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MHIRLISCPFIIINFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.7%; Score 1315.5; DB (
87.1%; Pred. No. 3.1e-92;
tive 11; Mismatches 18;
                   (BIOR-) BIOROAD GENE DEV LTD SHANGHAI
                                                                                                                                                                                                                     Claim 1; Page 27-28; 33pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM78328 standard; protein; 272 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243; Conservative
                                                                                         WPI; 2001-397948/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                          N-PSDB; AAH45131
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 272 AA;
                                                     Xie Y;
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Matches
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Human stem cell growth factor-like protein #4

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encoded polypeptides (AAM7832) AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, activity, tissue growth factor activity, hamminomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, in the diagnosis and/or infammation. Note: Records for SBO ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LPPVLERIGMEGIGYCLSSCPSGYYGTRYPDINKCTKCKVDCDTCPNKNPCTKCKSGPYL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LPFALERIGARQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCPNKNFCTKCKSGPYL 120
                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding polypeptides with cytokine-like activities, useful
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, Chen R, Wang ZW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MHLRLISCFFIILNFWEYIGSQNASRGRRQRRWHPNVSQGCQCCCATCSDYNGCLSCKPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to polynucleotides (AAK51456-AAK53435) and the
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                                                                                                                                                                                                                    Drmanac RT, Asundi V, Zhou P, X
Pang D, Wang J, Zhang J, Ren P,
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.7%; Score 1315.5; DB 87.1%; Pred. No. 3.1e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; Page 3214-3215; 6221pp; English.
                                                                                                                                                                                                                                       Wang D, Wang
Wejhrman T,
                                                                   19-JUL-2000; 2000US-00620325.
01-SEP-2000; 2000US-00654936.
1S-SEP-2000; 2000US-0065351.
20-CCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00728422.
                                                                                                                                                                                                                                                                                                                                                                      in diagnosis and gene therapy
                 03-PEB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
20-JUN-2000; 2000US-00598075.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 243; Conservative
                                                                                                                                                                                                                                                                                             WPI; 2001-476283/51.
N-PSDB; AAK51461.
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Ma Y, Zhao QA, Wo.
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                                                                                                                                                                                  (HYSE-) HYSEQ INC.
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The patent discloses novel stem cell growth factor-like proteins and polynucleotides encoding them. Proteins of the invention are also known as supporting factor for the proliferation of stem cells (SCR-1). Stem cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell, embryonic stem cell, germ cell, germ cell, embryonic stem cell, paematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell cultured using stem cell growth factor-like proteins can replace as a graft for the bone marrow transplantation or cord blood transplantation for treating a variety of diseases such as munuodeficiency syndrome, chonic granulomatous diseases, duplicated immunodeficiency syndrome, chonic as sickle cell anaemia Gaucher's disease, lysosomal storage such as sickle cell anaemia Gaucher's disease, lysosomal storage cellseases such as mucopolysactoral white matter degeneration, a variety of cancer and tumours. Proteins of the invention are useful for treating diseases such as parkhnon's diseases. Alzheimer's entered are useful for treating diseases such as Parkhnon's diseases.
                                Human; stem cell growth factor-like protein; antiinflammatory; nootropic; neuroprotective; vulnerary; cytostatic; anticonvulsant; immunostimulant; vasotropic; virucide; dermatological; tranquilliser; cerebroprotective; osteopathic; immunodeficiency syndrome; chronic granulomatous disease; duplicated immunodeficiency syndrome; wiskott-Aldrich syndrome; AIDS; acquired immunodeficiency syndrome; agammaglobulinaemia; thalassaemia; dancher's disease; lysosomal storage disease; mucopolysaccharidosis; adrenal white matter degeneration; anaemia; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; thrombocytopaenia; SCID; severe combined immunodeficiency; immune disorder; autoimmune disorder; autoimmune disorder; autoimmune pulmonary inflammation; cancer; tumour; gene therapy; SCR-1; supporting factor for the proliferation of stem cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel stem cell growth factor like polypeptides and polynucleotides for identifying modulators useful for treating diseases such as Alzheimer's disease, cancer, rheumatoid arthritis, osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22. .272 /note= "Human mature stem cell growth factor-like protein"
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in B, Dickson M, Mize NK, Nishikawa M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .21
/label=_Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUN-2000; 2000US-0215733P.
09-JAN-2001; 2001US-00757562.
05-FBB-2001; 2001US-0266614P.
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(KIRI ) KIRIN BEER KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-657166/75.
N-PSDB; AAD21728.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
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121 HIGKCLDSCPEGLEANNHTMECVSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDIL 180 QHPSAKGKGNLCPPTSETRTCIVQRKKCSKGERGKKGRERKRKKLNKEERKBTSSSSDSK 240 

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23.7 SLESSKRIPEQRENK--QQQKRRKVQDK-QKSVSVSTVH 272

AAB13168 standard; protein; 272 AA

28-JAN-2002 (first entry)

AAE13168;

RESULT 5
AAE13168
ID AAE1
XX
AC AAE1
XX
DT 28-J

241 GLESSIETPDQQENKERQQQQKRRARDKQQKSVSVSTVH 279

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Human, stem cell growth factor-like protein; antiinflammatory; nootropic; neuroprotective; vulnerary; cytostatic; anticonvulsant; immunostimulant; vasotropic; virucide; dermatological; tranquillierer; cerebroprotective; osteopathic; immunodeficiency syndrome; chronic granulomatous disease; duplicated immunodeficiency syndrome; wiskott-Aldrich syndrome; AIDS; acquired immunodeficiency syndrome; wiskott-Aldrich syndrome; AIDS; acquired immuno deficiency syndrome; agammaglobulinaemia; thalassaemia; Gaucher's disease; lysosomal storage disease; mucopolysaccharidosis; adrenal white matter degeneration; anaemia; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; thrombocytopaenia; SCID; severe combined immunodeficiency; immune disorder; autodimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; autoimmune pulmonary inflammation; cancer; tumour; gene therapy; SCR-1; supporting factor for the proliferation of stem cell.
                                                                                                                                                                                                              121 H.GKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII 180
                                                                                                                                                                                                                                                                                  HLGKCLDSCPEGLEANNHTMECVSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDIL 180
                                                                                                                                                                                                                                                                                                                                                   240
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inflammation. Sequences of the invention are also useful in gene therapy. The present sequence is stem cell growth factor-like protein from human
                                                                                                                                                                                 9
                                                                                                                                                                QHPSAKGKGNLCPPTSETRTCIVQRKKCSKGERGKKGRBRKRKKLNKEERKETSSSSDSK
                                                                                                                                                1 MHLRLISCPFIILNPMBYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR
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                                                                               85.7%; Score 1315.5; DB 4; Length 272; 87.1%; Pred. No. 3.1e-92; ive 11; Mismatches 18; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                   241 GLESSIETPDQQENKERQQQQKRRARDKQQKSVSVSTVH 279
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/label= Signal_peptide
22. .272
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2001US-00757562.
2001US-0266614P.
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                                                                             Query Match
Best Local Similarity 87.1%
Matches 243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                Sequence 272 AA;
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09-JAN-2001;
05-PEB-2001;
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The patent discloses novel stem cell growth factor-like proteins and polymucleotides encoding them. Proteins of the invention are also known as supporting factor for the proliferation of stem cells (SCR-1). Stem cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell, embryonic stem cell, germ cell, germ cell, embryonic stem cell, propentior cell, embryonic stem cell, propentior cell, manatopoietic progenitor cell, pluripotent cell or totipotent cell. The hacematopoietic progenitor cell, pluripotent cell or totipotent cell. The hacematopoietic progenitor cell, pluripotent cell or totipotent cell. The hacematopoietic progenitor cell, pluripotent cell or totipotent cell, cell, manatopoietic progenitor or cord blood transplantation for treating a variety of diseases uch as immunodeficiency syndrome, chronic granulomatous disease, duplicated immunodeficiency syndrome, chronic granulomatous (Miskott-Aldrich syndrome, acquired immune deficiency syndrome (AIDS), thalassaemia, hacemolytic anaemia due to enzyme defect, congenital anaemia cuch as sickhe cell anaemia Gaucher's disease, lyposomal storage diseases such as mucopolysaccharidosis, adrenal white matter degeneration, a variety of cancer and tunnours. Proteins of the invention cer useful for treating diseases uch as Parkinson's disease, Alzhaimer's disease and other neurodegenerative diseases, thrombocytopaenia, immune deficiency (SCID)) and autoimmune disorders such as multiple sclerosis, systemic lupus arythematosus, rheumatoid arthritis, and autoimmune plumonary chlumamation. Sequences of the invention are also useful in gene therapy.

The present sequence is stem cell growth factor-like protein from human
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                                                                                                                                                                                                                                       Novel stem cell growth factor like polypeptides and polynucleotides for identifying modulators useful for treating diseases such as Alzheimer's disease, cancer, rheumatoid arthritis, osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MHIRLISWIFIIINFWEYIGSQNASRGRRQRRWHPNV8QGCQGCATCSDYNGCLSCKPR
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                                                                                               Drmanac RT;
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                                                                                               Tang TY, Labat I, Tillinghast JS, Sinku A, Liu (
Stache-Crain B, Dickson M, Mize NK, Nishikawa M;
                                                                                                                                                                                                                                                                                                                                              Claim 28; Page 211-212; 232pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ź
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                       HYSBQ INC.
KIRIN BBER KK.
                                                                                                                                                                    WPI; 2001-657166/75.
N-PSDB; AAD21724.
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                    (HYSE-) )
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AC ABR6
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ABR62112;

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06-MAR-2003
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(MIZB/)
(NISH/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LABA/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to new stem cell growth factor-like polypeptides and polynucleotides. The stem cell growth factor-like polypeptides and polynucleotides are useful for inducing differentiation of embryonic and adult stem cells to give rise to different cell types, for treating e.g. cause the stem cells to give rise to different cell types, for treating e.g. leukaemia, haemophilia and degenerative diseases like Alzheimer's can disease. They are also useful for generating me tisuues and organs that may aid patients in need of transplanted tissues. The polynucleotides are useful as hybridisation probes, oligomers or primers for PCR, for chromosome and gene mapping, in recombinantly producing protein, in generating antisense DNA or RNA, in diagnostics as expressed sequence tags for identifying expressed genes, and for inducing immune response. The polypeptides are useful for generating antibodies that specifically bind the polypeptides are useful for generating antibodies that specifically bind the polypeptide source). Compositions comprising the current cor prevention of cancers, and other immunological disorders. The current cor prevention of cancers, and other immunological disorders. The current cor prevention of cancers, and other immunological disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QHPSAKGKGNLCPPTSETRTCIVQRKKCSKGERGKKGRERRRKKKLAKEERKETSSSSDSK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LPFVLERIGMKOIGVCLSSCPSGYYGTRYPDINKCTKCTVDCDTCFNKNPCTKCKSGFYL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New stem cell growth factor-like polypeptides and polynucleotides, useful for treating e.g. leukemia, hemophilia and degenerative diseases like Alzheimer's disease, and for inducing immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapa
                                                                 Human; secreted; stem cell growth factor; cytostatic; haemostatic; neuroprotective; immunostimulant; leukaemia; haemophilia; cancer; degenerative disease; Alzheimer's disease; food supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.7%; Score 1115.5; DB 6; Length 272; 87.1%; Pred. No. 3.1e-92; ive 11; Mismatches 18; Indels 7;
                                  Human clone 1 thrombospondin protein #23
                                                                                                                            immunological disorder; thrombospondin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Pig 1; 151pp; English
                                                                                                                                                                                                                                                                                                              30-AUG-2001; 2001US-0316368P.
10-DEC-2001; 2001US-0339739P.
19-APR-2002; 2002US-00125852.
                                                                                                                                                                                                                                                                           10-AUG-2002; 2002WO-US027746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 243; Conservative
18-AUG-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-381616/36.
                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 272 AA;
                                                                                                                                                                                                     WO2003029405-A2
                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                          10-APR-2003.
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22. .272 // Andrure stem cell growth factor-like protein. This protein is specifically claimed in claim 9"
181 QHPSA--KGNLCPPTNETRKCTVQRKKCQKGBRGKKGRBRKRKKPNKGBSKB--AIPDSK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stem cell growth factor-like protein; antianemic; anti-HIV; SCR-1; immunostimulant; vulnerary; haematopoietic stem cell; gene therapy; supporting factor for proliferation of stem cells; wound healing; haematopoietic progenitor cell; stromal cell; AIDS; thalassaemia; bone marrow transplantation; cord blood transplantation; chronic granulomatous disease; duplicated immunodeficiency syndrome; agammaglobulineamia; Hiskott-Aldrich syndrome; haemolytic anamia; congenital anaemia; dicklaemia; daucher's disease; morphogenesis; epithelial cell growth; ovarian follicle development; nerve cell growth; cartilage remodeling; bone growth; immunosuppression; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated stem cell growth factor-like polypeptide (referred as supporting factor for proliferation of stem cells (SCR-1) from mouse or human, or its mature protein portion, or ragment, analogue, variant or derivative, that retains stem cell growth factor activity. Also included are an isolated polymucleotide encoding SCR-1 (or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity, or the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated polypeptide having stem cell growth factor activity, useful for promoting wound healing, and as a medicine to proliferate or support human hematopoietic stem cells or human hematopoietic progenitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ပ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human stem cell growth factor-like protein, SCR 1 #4.
                                                                                 241 GLESSIETPDQQENKERQQQQKRRARDKQQKSVSVSTVH 279
                                                                                                                                                          237 SLESSKEIPEQRENK--QQQKKKKVQDK-QKSVSVSTVH 272

    .21
    /label= Signal_peptide

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                                                                                                                                                                                                                                                                                                                                                         ABO44432 standard; protein; 272 AA
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05-FEB-2001; 2001US-026614P.
05-APR-2001; 2001US-0282397P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-SEP-2003 (first entry)
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MIZE N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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CC SCR-1 polymucleotide, a host cell genetically engineered to comprising the SCR-1 polymucleotide, a host cell genetically engineered to comprising the SCR-1 polymucleotide in operative association with a regulatory sequence that controls expression of the polymucleotide in the host cell, the polymucleotide in the host cell, corporation of the polymucleotide in the host cell, corporation of the polymucleotide in the host cell, corporation of survival of haematopoietic stem cell activity to support proliferation or survival of haematopoietic stem cell comprise the as sequence appearing as ABO44433), an sequence does not comprise the as sequence appearing as ABO44433, an isolated SCR-1 polypeptide with stem cell growth factor activity and leaching any 10 consecutive ass from ABO44430, an isolated polypeptide (with stem cell growth factor activity having at least an as sequence appearing as ABO44432 and ABO44433, a nucleic acid array cell or germ cell, an anti-SCR_1 antibody, an uncleic acid array comprising the SCR-1 polymucleotide or a unique segment of the SCR-1 polymptide to maintain survival of or promote proliferation or survival of a stem cell or germ cell and an implant comprising a cell polymucleotide or express the SCR-1 polymptide to support proliferation or survival of a stem cell or germ cell and an implant comprising a cell comprision or survival of a stem cell or germ cell and an implant comprising wound the propertide and for maintening survival of or promoting wound chaing. The buman haematopoietic stem cell or promoting wound chaing. The buman haematopoietic stem cell or hamatopoietic comprised to a stem cell, a germ cell, a permention of haematopoietic stem cell or the composition or cord blood transplantation. The buman haematopoietic stem cell or human cell composition or transplantation or transplantation or transplantation or hearty for treating diseases such as chronic granicated immunodeficiency syndrome, assumaglobulinaemia, due to enzyme defect, compenition or such propertide is useful 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             morphogenesis, including tissue specific stem cell growth, epithelial cell growth and regulation, ovarian follicle development, promoting nerve cell growth, sustaining neuronal populations, cartilage remodeling, bone growth and immunosuppression. The present sequence is a Human SCR-1
complement of the polynucleotide), an (expression) vector comprising the
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Query Match 85.7%; Score 1315.5; DB 6; Length 272; Best Local Similarity 87.1%; Pred. No. 3.1e-92; Matches 243; Conservative 11; Mismatches 18; Indels 7; Sequence 272 AA;

LFFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYL 120 121 HIGKCLDNCPEGLEANNHTMECVSIVHCEVSEMNPWSPCTKKGKTCGFKRGTETRVREII 180 181 QHPSAKGKGNLCPPTSETRTCIVQRKKCSKGERGKKGRERKRKKLANKERKETSSSSDSK 240 181 QHPSA--KGNLCPPTWETRKCTVQRKKCQKGERGKKGRERKRKKDNKGESKB--AIPDSK 236 61 LPFVLERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCWVDCDTCFNKNPCTKCKSGFYL 120 121 HLGKCLDSCPEGLEANNHTWECVSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDIL 180 9 1 MHLRLISCPPIILNPMBYIGSQNASRGRRQRRMHPNVSQGCQGCATCSDYNGCLSCKPR 1 MHIRLISWIFILLNFWEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR 61 윱 δ 셤 Š 셤 è 셤

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ABO44413 standard; protein; 272 AA AB044413; RESULT 9 ABO44413 SXXX

(first entry) 30-SEP-2003 Human stem cell growth factor-like protein, SCR 1 #1

congenital anaemia; sicklaemia; Gaucher's disease; morphogenesis; epithelial cell growth; ovarian follicle development; nerve cell growth; cartilage remodeling; bone growth; immunosuppression; human. immunostimulant; vulnerary; haematopoietic stem cell; gene therapy; supporting factor for proliferation of stem cells; wound healing; haematopoietic progenitor cell; stromal cell; hIDS; thalassaemia; bone marrow transplantation; cord blood transplantation; chronic granulomatous disease; duplicated immunodeficiency syndrome; agammaglobulinaemia; Wiskott-Aldrich syndrome; haemolytic anaemia; Stem cell growth factor-like protein; antianemic; anti-HIV;

Homo sapiens.

JS2003044792-A1 

06-MAR-2003.

28-JUN-2001; 2001US-00894912.

28-JUN-2000; 2000US-0215733P. 05-FEB-2001; 2001US-0266614P. 05-APR-2001; 2001US-0282397P.

LABAT I. DRMANAC R T. TANG Y T. (TANG/) LABA/

MIZE N. (DRMA/) (MIZE/)

NISHIKAWA M GHA C (NISH/) (CHAO/) Mize N, Nishikawa M, lang YT, Labat I, Drmanac RT,

Chao C; N-PSDB; ACH04323, ACH04324. WPI; 2003-625403/59

Novel isolated polypeptide having stem cell growth factor activity, useful for promoting wound healing, and as a medicine to proliferate or support human hematopoietic stem cells or human hematopoietic progenitor cells.

Claim 23; Fig 3; 96pp; English.

Gaps 7; The invention relates to an isolated stem cell growth factor-like polypeptide (referred as supporting factor for proliferation of stem cells (SCR-1) from mouse or human, or tem mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity. Also included are an isolated polynucleotide encoding SCR-1 (or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity, or the complement of the polynucleotide), an (expression) vector comprising the SCR-1 polymcleotide, a host cell genetically engineered to contain the SCR-1 polymcleotide in the host cell, that controls expression of the polymcleotide in the host cell, preparation of the SCR-1 polymcleotide in the host cell, preparation of the SCR-1 polymcleotide (the polypeptide having an activity to support proliferation or survival of haematopoietic stem cell or haematopoietic progenitor cell, with a proviso that C-terminal as sequence does not comprise the as sequence appearing as ABO44431, an isolated SCR-1 polypeptide with stem cell growth factor activity and lacking any 10 consecutive and from ABO44430, an isolated polypeptide appearing as ABO44428 and ABO44429, a culture medium comprising the SCR-1 cell or germ cell, an anti-SCR 1 antibody, an uncleic acid artary. celfor germ cell, an anti-SCR I antibody, a nucleic acid array comprising the SCR-1 polynucleotide or a unique segment of the SCR-1 polynucleotide attached to a surface, a stronal cell genetically engineered to express the SCR-1 polypeptide to support proliferation of survival of a stem cell or germ cell and an implant comprising a cell genetically engineered to express the SCR-1 polypeptide to support WO200177169-A2

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proliferation or survival of a stem cell or germ cell. The SCR-1

polypeptide is useful for identifying a compound that binds to the SCR-1

colypeptide and for maintaining survival of or promoting proliferation of

a stem cell, a germ cell, a haematopoietic stem cell or a haematopoietic

progenitor cell. The SCR-1 polypeptide is useful for promoting wound

consenior cell. The SCR-1 polypeptide is useful for promoting wound

consenior cell culture using the SCR-1 polypeptide can replace as a

graft for the conventional bone marrow transplantation or cord blood

cransplantation. The transplantation of haematopoietic stem cells can be

cransplantation. The transplantation of haematopoietic stem cells can be

cransplantation. The transplantation or sord blood

cransplantation. The transplantation or cord blood

cransplantation. The transplantation or cord blood

diseases, duplicated immunodeficiency syndrome, agammaglobulinaemia,

diseases, duplicated immunodeficiency syndrome, agammaglobulinaemia,

due to enzyme defect, congenital anaemia such as sicklaemia, Gaucher's

disease etc. the SCR-1 polypeptide is useful for cell growth and

cransplantation, ovarian follicle development, promoting nerve

cell growth and regulation, ovarian follicle development, promoting nerve

cell growth, austaining neuronal populations, cartilage remodeling, bone

proved.
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Sequence 272 AA;

61 LPPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCRADCDTCFNKNFCTKCKSGFYL 120 61 LPFVLERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKVDCDTCFNKNPCTKCKSGFYL 120 HIGKCLDSCPEGLEANNHTMECVSIVHCEASEWSPWSPCMKKGKTCGPKRGTETRVRDIL 180 121 HLGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGPKRGTETRVREII 180 OHPSAKGKGNI,CPPTSETRTCI VORKKCSKGERGKKGRERKRKKLINKEERKETSSSSDSK 240 QHPSA--KGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGBSKB--AIPDSK 236 9 9 1 MHLRLISCFFIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR 1 MHLRLISWLFIILNFWEYIGSQNASRGRRQRRMHPNVSQGCQGCATCSDYNGCLSCKPR Gaps 7; Query Match 85.7%; Score 1315.5; DB 6; Length 272; Best Local Similarity 87.1%; Pred. No. 3.1e-92; Matches 243; Conservative 11; Mismatches 18; Indels 7; 237 SLESSKEIPEQRENK--QQQKKRXVQDK-QKSVSVSTVH 272 241 GLESSIETPDQQENKERQQQQKRRARDKQQKSVSVSTVH 279 181 121 181 g 셤 ઠે 셤 ે è 셤 ઠે 셤

AAE13151 standard; protein; 273 AA AAB13151; RESULT 10 AAE13151 

28-JAN-2002 (first entry)

Human stem cell growth factor-like protein #3.

Human; stem cell growth factor-like protein; antiinflammatory; nootropic; neuroprotective; vulnerary; cytostatic; anticonvulsant; immunostimulant; vasotropic; virucide; dermatological; tranquilliser; cerebroprotective; osteopathic; immunodeficiency syndrome; chronic granulomatous disease; duplicated immunodeficiency syndrome; chronic granulomatous disease; acquired immunodeficiency syndrome; agammaglobulinaemia; thalassaemia; adveber; a disease; lysosomal storage disease; ucopolyasocharidosis; adrenal white matter degeneration; anaemia; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; thrombocytopaenia; SCID; severe combined immunodeficiency; immune disorder; autoimmune disorder; multiple sclerosis; systemic luque erythematosus; rheumatoid arthritis; autoimmune pulmonary inflammation; cancer; tumour; gene therapy; SCR-1; supporting factor for the proliferation of stem cell.

Homo sapiens

182 183

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The patent discloses novel stem cell growth factor-like proteins and polymucleotides encoding them. Proteins of the invention are also known as supporting factor for the proliferation of stem cells (SCR-1). Stem cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell, embryonic stem cell, grem cell, grem cell, growth factor-like proteins are useful for supporting proliferation or cell, grem line stem cell, embryonic stem cell, paematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell cultured using stem cell growth catorial seases such as immunodeficiency syndrome, chronic granulomatous confiseases udplicated immunodeficiency syndrome, chronic granulomatous wiskott-Aldrich syndrome, acquired immune deficiency syndrome, lulbS), thalassaemia, haemolytic anaemia due to enzyme defect, congenital anaemia cultassaemia, haemolytic anaemia due to enzyme defect, congenital anaemia cells as sickle cell anaemia due to enzyme defect, congenital anaemia desensation, a variety of cancer and tumours. Proteins of the invention cere useful for treating diseases such as Parkinson's disease, harbeimer's clisease and other neurodegenerative diseases, thrombocytopaenia, immune deficiencies and disorders such as severe combined immunodeficiency (SCID) and autoimmune disorders such as multiple selezois, systemic lupus erythematosus, rheumatoid arthritis, and autoimmune pulmonary inflammation. Sequence is stem cell growth factor-like protein from human
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel stem cell growth factor like polypeptides and polynucleotides for identifying modulators useful for treating diseases such as Alzheimer's disease, cancer, rheumatoid arthritis, osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIRLISWLFIIINFWEYIGSQNASRGRRQRRWHPNVSQGCQGGGATCSDYNGCLSCKPRL
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                                                                                                                                                                                                                                                                                                          Liu C,
                                                                                                                                                                                                                                                                                                        Labat I, Tillinghast JS, Sinku A, Liu (
ain B, Dickson M, Mize NK, Nishikawa M;
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                                                                                                                              05-APR-2000; 2000US-00543774.
28-JUN-2000; 2000US-0215733P.
09-JAN-2001; 2001US-00757562.
05-FEB-2001; 2001US-0266614P.
                                                                                    05-APR-2001; 2001WO-US011208
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Matches 242; Conservative
                                                                                                                                                                                                                                           (HYSB-) HYSEQ INC.
(KIRI ) KIRIN BEER KK.
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N-PSDB; AAD21725.
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                                              18-OCT-2001
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The invention relates to an isolated stem cell growth factor-like polypeptide (referred as supporting factor for proliferation of stem cells (SCR-1)) from mouse or human, or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity. Also included are an isolated polymucleotide encoding SCR-1 (or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity, or the complement of the polymucleotide, an (expression) vector comprising the SCR-1 polymucleotide, an operative association with a regulatory sequence or strain polymucleotide in operative association with a regulatory sequence that controls expression of the polymucleotide in the host cell, that controls expression of the SCR-1 polymucleotide in the host cell, caprassion product of the SCR-1 polymucleotide (the polypeptide having an activity to support proliferation or survival of haematopoietic stem cell or heamatopoietic stem cell or heamatopoieti
                                                                                                                                                                                                                                                                                                                                                                                                                                 immunostimulant; vulnerary; hematopoletic stem cell; gene therapy; supporting factor for proliferation of stem cells; wound healing; supporting factor for proliferation of stem cells; wound healing; hematopoletic progenitor cell; stromal cell; hibs; thalassaemia; bone marrow transplantation; cord blood transplantation; chronic granulomatous disease; duplicated immunodeficiency syndrome; agammaglobulinaemia; Miskott-Aldrich syndrome; haemolytic anaemia; congenital anaemia; sicklaemia; Gaucher's disease; morphogenesis; epithelial cell growth; ovarian follicle development; nerve cell growth; cartilage remodeling; bone growth; immunosuppression; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated polypeptide having stem cell growth factor activity, useful for promoting wound healing, and as a medicine to proliferate or support human hematopoietic stem cells or human hematopoietic progenitor
                                                                                                                                                                                                                                                                                                                                                                                                                Stem cell growth factor-like protein; antianemic; anti-HIV; SCR-1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fang YT, Labat I, Drmanac RT, Mize N, Nishikawa M,
                                                                                                                                                                                                                                                                                                                                                          Human stem cell growth factor-like protein, SCR 1 #2.
242 LESSIBTPDQQENKERQQQQKRRARDKQQKSVSVSTVH 279
                            Claim 23; Page 72-73; 96pp; English.
                                                                                                                                                                                           ABO44414 standard; protein; 273 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUN-2000; 2000US-0215733P.
05-FEB-2001; 2001US-0266614P.
05-APR-2001; 2001US-0282397P.
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DRMANAC R T.
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NISHIKAWA M.
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(NISH/)
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                                                                                                                                     RESULT 11
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cc isolated SCR-1 polypeptide with stem cell growth factor activity and lacking any 10 consecutive aas from ABO4430, an isolated polypeptide with stem cell growth factor activity having at least an as sequence appearing as ABO44428 and ABO44430, a culture medium comprising the SCR-1 polypeptide to maintain survival of or promote proliferation of a stem cell, an anti-SCR lantibody, a mucleic acid array comprising the SCR-1 polymuclecided or a unique segment of the SCR-1 polymuclecided extached to a surface, a stromal cell genetically comprising the SCR-1 polymuclecided or a unique segment of the SCR-1 polymuclecided at a stem cell or germ cell and an implant comprising a cell contributed or survival of a stem cell and an implant comprising a cell contributed by engineered to express the SCR-1 polypeptide to support proliferation or survival of a stem cell or germ cell. The SCR-1 polypeptide is useful for promoting proliferation or survival of a stem cell or germ cell. The SCR-1 polypeptide is useful for promoting wound a stem cell, a germ cell, a hemantopoietic stem cell or a haematopoietic stem cell or a haematopoietic stem cell or promoting wound correspondent or cell culture using the SCR-1 polypeptide can replace as a graft for the conventional bone marrow transplantation or cord blood cransplantation. The transplantation of haematopoietic stem cells can be employed as a therapy for treating diseases such as chornic granulomatous diseases, duplicated immunodeficiency syndrome, agammaglobulinemia, cumphogenesis, including tissue specific stem cell growth, and regulation, ovarian follicle development, promoting nor properior cell growth and immunosuppression. The present sequence is a Human SCR-1 polypeptide is useful for cell growth and immunosuppression. The present sequence is a Human SCR-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.4%; Score 1310.5; DB 6; Length 87.1%; Pred. No. 7.5e-92; ive 11; Mismatches 18; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW85607 standard; protein; 292 AA
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242; Conserv
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Matches 24
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Homo sapiens

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vasotropic, virucide, dermatological; tranquilliser; cerebroprotective
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                                                                                                                                                                                                                                                                                  of clones ci254 (AAV83132), da2286 (AAV83133), du4105 (AAV83134), el801 (AAV83134), el801 (AAV83135), er5691 (AAV83136), fhl235 (AAV83137), fm601 (AAV83139) or fr4732 (AAV83139), (all clones are deposited as ArCC 98415) and the proteins they encode are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical activity, immune system boosting activity. The polymucleotides are also believed to be useful for gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 QHPSA--KGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKDNKGESKE--AIPDSK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; stem cell growth factor-like protein; antiinflammatory; nootropic; neuroprotective; vulnerary; cytostatic; anticonvulsant; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                     New polynucleotides encoding secreted human proteins - are derived from human foetal brain, adult brain, adult blood or placenta cDNA libraries, useful, e.g. as potential immunomodulators.
                                                                                                                                                                                                                                                                         The nucleotide sequence (NS) of the full-length protein-coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MHLRLISCPFILLNPMBYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MELIZI SWILFI I LINPWEYI GSQNASRGRRQRRWHPNVSQCQGGCATCSDYNGCLSCKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPPVLER I GMKQ1 GVCLSSCPSGYYGTRYPD1NKCTKCKVDCDTCFNKNFCFKCKSGFYL
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                     Treacy M;
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9
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                                                                                                                                     Lavallie ER, Racie LA, Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 GLESSIETPDQQENKERQQQQKRRARDKQQKSVSVS 276
                                                                                                                                                                                                                                                    Claim 8; Page 63-64; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE13170 standard; protein; 292 AA.
                                                          98WO-US008336.
                                                                              97US-00845296
98US-00065125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human SCR-1 related protein.
                                                                                                                                       Jacobs K, Mccoy JM, Lava
Spaulding V, Agostino MJ;
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                                                                                                               (GEMY ) GENETICS INST INC
                                                                                                                                                                       WPI; 1999-024059/02.
                                                                                                                                                                                 N-PSDB; AAV83133
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 292 AA;
                                                        24-APR-1998;
              WO9849302-A1
                                                                               25-APR-1997;
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                                                                                           23-APR-1998;
                                   05-NOV-1998
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The patent discloses novel stem cell growth factor-like proteins and polymucleotides encoding them. Proteins of the invention are also known as supporting factor for the proliferation of stem cells (SCR-1). Stem cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell, embryonic stem cell, paramatopoietic stem cell, embryonic stem cell, paramatopoietic stem cell, embryonic stem cell, paramatopoietic stem cell. pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic stem replace as a grafe for the bone marrow cell. The proteins can replace as a grafe for the bone marrow or factor-like proteins can replace as a grafe for the bone marrow cord blood transplantation for treating a variety of diseases such as immunodeficiency syndrome, chronic granulomatous disease, duplicated immunodeficiency syndrome, chronic granulomatous conflicts and immunodeficiency syndrome, plusplantation as sickle cell anaemia due to enzyme defect, congenital anaemia cuch as micopolysaccharidosis, adrenal white matter degeneration, a variety of cancer and tumours. Proteins of the invention are useful for treating diseases uch as Parkinson's disease, harbeimer's disease and other neurodegenerative diseases, thrombocytopaenia, immune deficiencies and disorders such as severe combined immunodeficiency (SCID) and autoimmune disorders such as multiple solerois, systemic lupus erythematosus, rheumatoid arthritis, and autoimmune pulmonary inflammation. Sequence of the invention are also useful in gene therapy. The present sequence is human SCR-1 related protein
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osteogathic; immunodeficiency syndrome; chronic granulomatous disease; duplicated immunodeficiency syndrome; Wiskott.Aldrich syndrome; AIDS; acquired immune deficiency syndrome; wiskott.Aldrich syndrome; AIDS; daucher's disease; lysosomal storage disease; mucopolysaccharidosis; adrenal white matter degeneration; anaemia, neurodegenerative disease; Parkinson's disease; thrombocycopaemia; SCID; severe conbined immunodeficiency; immune disorder; autorimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; supporting factor for the proliferation of stem cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel stem cell growth factor like polypeptides and polynucleotides for identifying modulators useful for treating diseases such as Alzheimer's disease, cancer, rheumatoid arthritis, osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Gaps
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84.2%; Score 1293; DB 4; Length 292;
Best Local Similarity 85.1%; Pred. No. 1.7e-90;
Matches 235; Conservative 14; Mismatches 21; Indels 6
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Stache-Crain B, Dickson M, Mize NK, Nishikawa M;
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28-UN-2000; 2000US-0215739P.
09-UN-2001; 2001US-0057562.
05-PBB-2001; 2001US-0266614P.
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(KIRI ) KIRIN BEER KK.
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N-PSDB; AAD21740.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
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61 LPFALERIGAKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYL 120
                                                                                                                 HIGKCLDNCPEGLEANNHTWECVSIVHCEVSEWNPWSPCTKKGKTGGFKRGTETRVREII 180
                                                                                                                                                                                121 HLGKCLDSCPEGLEANNHTMECVSIVHCEASEMSPWSPCMKKGKTCGFKRGTETRVRDIL 180
                                                                                                                                                               181 QHPSAKGKGNLCPPTSETRTCIVQRKKCSKGERGKKGRERKRKKLNKKERKETSSSSDSK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human secreted or transmembrane protein (1), their fragments and is encoded by specific complementary deoxyribonucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cytostatic; antirheumatic; antiarthritic; vulnerary; analgesic; antinflammatory; antibacterial; immunosuppressive; antiparkinsonian; neuroprotective; noctropic; osteopathic; haemostatic; vasotropic; antiulcer; fungicide; antidiabetic; antiasthmatic; antiallergic; antiulcer; fungicide; antidiabetic; actiasthmatic; antiallergic; immunostimulant; antiparasitic; secreted protein; transmembrane protein; cytokine; cell proliferation; cell differentiation; autoimmune disease; stem cell; growth factor; nervous system disease; neuropathy; Alzheimer's disease; Parkinson's disease; huntington's disease; osteoporosis; severe combined immunodeficiency; SCID; infection; multiple sclerosis; rheumatoid arthritis; gene therapy.
1 MHLRLISWLFIILNFWEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel secreted or transmembrane protein and polymucleotide encoding the protein, useful for diagnosis and treatment of neurological disorders, cancer, autoimmune diseases, bone disorders and lung or liver fibrosis.
                                LPPVLERICAKQIGVCLSSCPSGYYGTRYPDINKCTKCKVDCDTCFNKNFCTKCKSGFYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collins-Racie LA, Evans C;
                                                                                                                                                                                                                                241 GLESSIETPDQQENKERQQQQKRRARDKQQKSVSVS 276
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Spaulding V;
                                                                                                                                                                                                                                                                                                                                                  ABP61846 standard; protein; 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polypeptide SEQ ID NO 200.
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MCCOY J M.
LAVALLIE E R.
COLLINS-RACIE L A.
EVANS C.
                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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(MERB/)
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cocker mammalian proteins (II) where the procesn is abusernially treating or ameliorating a medical condition, especially immunological treating or ameliorating a medical condition, especially immunological treatment or prevention of tumours: (I) eshibite activity relating to angiogenesis, cytokine, cell proliferation, cell differentiation, antiinflammatory, stem cell growth factor activity and activin or inhibin-related cytokine, cell proliferation, cell differentiation or inhibin-related cells frow be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. (I) induces the proliferation of neural cells and central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease and commoniation of hematopoiesis and is useful for treating myeloid cell disorders, platelet disorders such as thrombocytopaenia and for regemeration of bone, cartilage, tendon, ligament and/or nerve tissue growth and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders or cegeneration and treatment of lung or liver fibroals, reperfusion injury in various tissues, various immune deficiencies and disorders including cevere combined immunodeficiency (SCID), bacterial or fungal lifections, autoimmune disorders e.g. multiple spreaded and in gene therapy. The present cecombinant protein, as markers for tissues in which the corresponding protein is preferentially expressed and in gene therapy. The present
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(cDNA) inserts (II), where the protein is substantially free from
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85.1%; Pred. No. 1.7e-90;
tive 14; Mismatches 21;
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Matches 235; Conservative
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Homo sapiens

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The invention relates to new stem cell growth factor-like polypeptides and polynucleotides. The stem cell growth factor-like polypeptides and polynucleotides are useful for inducing differentiation of embryonic and adult stem cells to give rise to different cell types, for treating e.g. leukaemia, haemophilia and degenerative diseases like Alzheimer's consease. They are also useful for generating new tissues and organs that can apply and patients in need of transplanted tissues. The polymclectides are useful as hybridisation probes, oligomers or primers for PCR, for chromosome and gene mapping, in recombinantly producing protein, in generating antisense DNA or RNA, in diagnostics as expressed sequence tags for identifying expressed genes, and for inducing immune response. The polypeptides are useful for generating antibodies that specifically bind the polypeptides are useful for generating antibodies that specifically bind the polypeptides as molecular weight markers, and as a food supplement (e.g. protein or amino acid supplement, and as a carbon, nitrogen or carbohydrate source). Compositions comprising the current polypeptides or polynucleotides are useful for the diagnosis, treatment or prevention of cancers, and other immunological disorders. The current sequence represents a human secreted protein clone da_288_6
                                                                                                                                                                                                                                                                                                                                                  New stem cell growth factor-like polypeptides and polymucleotides, useful for treating e.g. leukemia, hemophilia and degenerative diseases like Alzheimer's disease, and for inducing immune response.
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                                                                                                                                          30-AUG-2001; 2001US-0316368P-
10-DEC-2001; 2001US-0339739P-
19-APR-2002; 2002US-00125852.
                                                                                                   30-AUG-2002; 2002WO-US027746
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                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
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                                                            10-APR-2003
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completed: June 29, 2004, 16:59:52

time : 51.7836 secs

Search Job tim

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Query Match
Best Local Similarity 23.33
Matches 56; Conservative
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US-08-284-941-2
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-525-940-18
US-08-976-838-18
US-08-976-838-18
US-09-214-5558-7
US-08-22-940-15
US-08-22-940-15
US-08-22-940-15
US-08-22-0218-14
US-07-862-0218-14
US-07-862-0218-14
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US-08-447-642-2
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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FILING UNIT 3 AUGUST 1394 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: NEELEY PH.D., RICHARD L. REGISTRATION NUMBER: 30092 REFERENCE/DOCKET WWHERE: CHIR-009/01US TELECOMMUNICATION INFORMATION:
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12;

Gaps

72;

11.7%; Score 179; DB 2; Length 969; 23.3%; Pred. No. 1.2e-07; Live 23; Mismatches 89; Indels

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US-09-236-503-2
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CLSSCPSGYYGTRYPDINKCTKCKVDCDTCPNK-NPCTKCKSGFYLHLGKCLDSCPEGLE 134
                                                                                                                                                                   ---PWSP 158
                                                                                                                                                                                                                                                                                                                                                                                                      898 CRRCDENCLSCAGSSRNCSRCKTGFTQLGTSCITNHTCSNADETFCEMVKSNRLC--ERK 955
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Patent No. 5989890
GENERAL INFORMATION:
APPLICANT: BARK, HILLIP J
APPLICANT: KIEFER, MICHAEL C
TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: COOLEY GODWARD CASTRO HUDDLESON & TATUM
STREET: FIVE PALO ALTO SQUARE
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11.7%; Score 179; DB 2; Length 969;
Best Local Similarity 23.3%; Pred. No. 1.2e-07;
Matches 56; Conservative 23; Mismatches 89; Indels
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MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,642
PILING DATE: 23-MAY-1995
CLASSIFICATION: A24
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/284,941
PILING DATE: 2 August 1994
ATTORNEY/AGRNT INFORMATION:
NAME: NEELEY PH.D., RICHARD L.
REGISTRATION NUMBER: 30092
REGISTRATION NUMBER: 30092
REGISTRATION NUMBER: 30092
REGISTRATION NUMBER: GHIR-009/01US
TELECOMMUTCATION INFORMATION:
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US-08-447-642-2
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GENERAL INFORMATION:
APPLICANT: Barr, Philip J
APPLICANT: Barr, Philip J
APPLICANT: Refer, Michael C
APPLICANT: Kefer, Michael C
TITLE OF INVENTION: Compositions and Methods for PACE 4 and 4.1 Gene and
TITLE OF INVENTION: Compositions in Cells
FILE REPRENCE: CHIR-009/04US
CURRENT PELING DATE: 1999-01-25
EARLIER APPLICATION NUMBER: 08/47,642
EARLIER APPLICATION NUMBER: 08/284,941
EARLIER PILING DATE: 1995-05-23
EARLIER PILING DATE: 1994-08-02
EARLIER PILING DATE: 1994-08-02
EARLIER APPLICATION NUMBER: 07/848,629
EARLIER PILING DATE: 1994-03-09
NUMBER: OF SEQ ID NOS: 162
159 CMKKGKTC----GFKRG-----TETRVRDILQHPSAKGKGNLCPPTSETRTCIVQRK 206
                                                                    737 YPGDTAARRCRR-----CHKGCETCSSRAATQCLSCR-RGFY-----HHQEMNT 779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US93-02147A-2;
Sequence 2, Application PC/TUS9302147A
Sequence 2, Application PC/TUS9302147A
Sequence 2, Application PC/TUS9302147A
Sequence 2, Application PCT-US9302147A
Sequence 2, Application PCT-USP PCT-USP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09236503
Patent No. 6277590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 23.3%
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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799 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        780 CVTLCPAGPYADE--SOKNCLKCHPSCKKCVDEPEKCTVCKEGFSLARGSCIPDCEPGTY 837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Patent No. 569183;
GENERAL INPORMATION:
Franzusoff, Alex
PPLICANT: Franzusoff, Alex
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
TITLE OF INVENTION: ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5; Length 969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 ANNHTMBC------VSIVHCBAS----EWS----
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368,852
FILING DATE: 05-JAN-1995
CLASSIFICATION: 435
ATTORNEY AGENT INPORMATION:
NAME: Verser, Carol Talkington
Patentin Release #1.0, Version #1.25
               CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02147A
FILING DATE: 19930309
CLASSIPCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,629
FILING DATE: 09-WAR-1992
APPLICATION NUMBER: US 07/848,629
FILING DATE: 09-WAR-1992
ATTORNEY/AGENT INPORMATION:
REGISTRATION NUMBER: 30092
REFERENCE/DOCKET NUMBER: GHIR-009/00US
TELECHONGUNI CATION INPORMATION:
TELEPHONE: (415) 494-7622
TELEPHONE: (415) 494-7622
TELEPHONE: (415) 857-0663
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 23.3%; Pred. No. 1.2e-Matches 56; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 969 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 80203
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SOPTWARE:
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S9 KRCRKCAPNCESCFGSHGDQCMSCKYGYFLMBETNSCVTHCPDGSYQDTKKNLC----- 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 PRCSEVGCDGPGPDHCND---CL----HYYYGLK----NNTRICVSSCPPGHY---HADK 58
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                                                                                                                                                                                                                                                                                                                                                                                                             42; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23, Application US/08525940

Batent No. 5866351

GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
APPLICANT: Miranda, Luis R.
APPLICANT: World, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES
TITLE OF INVENTION: ENCODING SAID PROTEASES
NUMBER OF INVENTION: ENCODING SAID PROTEASES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                             57; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/525,940
                                                                                                                                                                                                                                                                                                                                                       ; Score 155; DB 1; 
; Pred. No. 4e-06; 
23; Mismatches :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3: Sheridan Ross & McIntosh
1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 08/368,852
FILING DATE: 01-JAN-1995
PRIOR APPLICATION UNDER: US 08/088,322
APPLICATION WUMBER: US 08/088,322
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INPORMATION:
NAME: Connell, Gary J.
REGISTATION UNDER: 32,020
REPRENCE/DOCKET NUMBER: 2848-11-C1
TELECOMMUNICATION INPORMATION:
REGISTRATION NUMBER: 37,459
REFERENCS/POCKET NUMBER: 2848-11
TELECOMMUNICATION INFORMATION:
TELECOMMUS: 303/863-9700
                                                                                                                                                                                                                                                                                                                                                       10.14;
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TELEPAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 23
SEQUENCE CHARACTERISTICS:
                                                                                                   TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 28.2%
Matches 48; Conservative
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; MOLECULE TYPE: protein
US-08-368-852-15
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Ploppy disk
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MEDIUM TYPE: Floppy
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
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STATE: Colora
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US-08-976-838-21
                                                                                                                                              US-08-525-940-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 PNVSQ-GCQG-GCATCSDYNGCLSCKPRLFFVLERIGMKQIGVCLSSCPSGYYGTRYPDI 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 23, Application US/08976838
Patent No. 5981259
GENERAL INPORMATION:
GENERAL INPORMATION:
GENERAL INPORMATION:
GENERAL INPORMATION:
TITLE OF INVENTION:
OF INVENTION:
MUMBER OF SEQUENCES:
ADDRESSER:
ADDRESSER:
Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
                                                                                                      10.0%; Score 154; DB 2; Length 799; 28.2%; Pred. No. 1.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Picture PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,838
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.0%; Score 154; DB 2; 28.2%; Pred. No. 1.6e-05; tive 23; Mismatches 57;
                                                                                                                                                23; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFRENCE/DOCKET NUMBER: 2848-
TELECOMMUNICATION INFORMATION:
TELEPHOR: (303) 863-9700
TELEFAX: (303) 863-9700
TELEFAX: (303) 863-9700
TELEFAX: (393) 863-9700
                                                                                                                                                  48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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MOLECULE TYPE: protein

US-08-976-838-23
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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Best Local Similarity
                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Colorado COUNTRY: U.S.A.
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US-08-976-838-23
                                                               US-08-525-940-23
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                                                                                                                                                  Matches
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606 PECSEVGCDGPGPDHCND---CL----HYYYKLK----NNTRICVSSCPPGHY---HADK 651
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------GSRCSVSCB 658
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149 EASEWSPWSPCMKKGKTC-GFKRGTETRVRDILQHPSAKGKGNLCPPTSE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 881;
                                                                                                                                                                                                                                           APPLICANT: Prazusoff, Alex
APPLICANT: Miranda, Luis R.
APPLICANT: Miranda, Luis R.
APPLICANT: Wolf, JOSeph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
TITLE OF INVENTION: ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                      -----RKCSENCKTCTEFHNCTECRDGLSLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,852
FILING DATE: 01-JAN-1995
PRIOR APPLICATION DATA: US 08/088,322
PRIOR APPLICATION NUMBER: US 08/088,322
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: CONNELL, GALY J.
REGISTRATION WUMBER: 28,48-11-C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/08/525,940
PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                     Sequence 21, Application US/08525940
Patent No. 5866351
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 NKCTKCKVDCDTCFNK--NFCTKCKSGFYLH--LGKCLDSCPEGLEANNHTMECVSIVHC 14B
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                                           GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
TITLE OF INVENTION: COA+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
10.0%; Score 154; DB 2; Length 881;
Best Local Similarity 28.2%; Pred. No. 1.8e-05;
Matches 48; Conservative 23; Mismatches 57; Indels
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Patent No. 5866351

GENERAL INFORMATION:
APPLICANT: Pranzusoff, Alex
APPLICANT: Miranda, Luis R.
APPLICANT: Wolf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,838
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 28.020
REFREENCE/DOCKET NUMBER: 2848-11-C2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                           ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 21, Application US/08976838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 881 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-976-838-21
                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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STATE: Colorado
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ZIP: 80203
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    640 PECSEVGCDGPGPDHCND---CL----HYYYKLK----NNTRICVSSCPPGHY---HADK 685
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                                                                                                                                                                                                                                                                                                    Query Match 10.0%; Score 154; DB 2; Length 915; Best Local Similarity 28.2%; Pred. No. 1.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.0%; Score 154; DB 4; Length 915; 28.2%; Pred. No. 1.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57; Indels
                                                                                                                                                                                                                                                                                                                                              57; Indels
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APPLICANT: INSTITUT DE RECHERCHE CLINIQUE DE MONTRAL

ITILE OF INVENTION: PRO-PROTEIN CONVERFING
FILLE REFERENCE: PRO-PROTEIN CONVER ENZ

CURRENT PILING DATE: 1999-01-04

PRIOR APPLICATION NUMBER: 60/021,008

PRIOR APPLICATION NUMBER: 2,203,745

PRIOR PILING DATE: 1996-07-26

PRIOR PILING DATE: 1997-04-25

NUMBER OF SEQ ID NOS: 9

SOPTWARE: PARCENTIN VOINGE: 9
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                                                                                                                                                                                                                                                                                                                                              23; Mismatches
RESISTANTION NUMBER: 32,020
RESISTANTION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C2
TELEPHONICATION INPORMATION:
TELEPHONE: (303) 863-0723
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHRAACTERISTICS:
LENGTH: 915 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09214555B Patent No. 6380171
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                                                                                                                                                                                                                                                                                                                                              48; Conservative
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LENGTH: 915

TYPE: PRT

COGGANISM: Homo sapiens

US-09-214-5558-2
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Best Local Similarity
                                                                                                                                                                                                                  TOPOLOGY:
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US-09-214-555B-7
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640 PECSEVGCDGPGPDHCND----CL----HYYYKLK----NNTRICVSSCPPGHY----HADK 685
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APPLICANT: Franzusoff, Alex
APPLICANT: Miranda, Luis R.
APPLICANT: Wolf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES
TITLE OF INVENTION: ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57; Indels
GENERAL INPORATION:
APPLICANT: INSTITUT DE RECHERCHE CLINIQUE DE MONTRAL
TITLE OF INVENTION: PRO-PROTEIN CONVERTING ENZYME
FILE REPRENEUE: PRO-PROTEIN CONVER ENZ
CURRENT APPLICATION NUMBER: US/09/214,555B
CURRENT PILING DATE: 1999-01-04
PRIOR APPLICATION NUMBER: 60/021,008
PRIOR APPLICATION NUMBER: 2,203,745
FRIOR AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.0%; Score 154; DB 4; 28.2%; Pred. No. 1.9e-05; tive 23; Mismatches 57,
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REFERENCE/DOCKET NUMBER: 2848-11-C1
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FILING DATE: 01-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/088,322
FILING DATE: 07-UUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-525-940-15; Sequence 15, Application US/08525940; Patent No. 5866351
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Best Local Similarity 28.2
Matches 48; Conservative
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1700 Lir
CITY: Denver
STATE: Colorado
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 NKCTKCKVDCDTCFNK--NPCTKCKSGPYLH--LGKCLDSCPEGLEANNHTMECVSIVHC 148
                                                                                                                                                                                                                                                                                                                                                                            13 PECSEVGCDGPGPDHCND---CL---HYYYKLK----NNTRICVSSCPPGHY---HADK 58
                                                                                                                                                                                                                                                                                                                                               35 PNVSQ-GCQG-GCATCSDYNGCLSCKPRLPFVLERIGMKQIGVCLSSCPSGYYGTRYPDI
                                                                                                                                                                                                                                                                                                  53; Indels 48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 EASEWSPWSPCMKKGKTCGFKRGTB----TRVRDILQHPSAKGKGNLCPPTSB 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/08976838
Patent No. 5981259
GENERAL INFORMATION:
APPLICANT: Prantausoff, Alex
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF INVENTION: 31
CORRESPONDENCE ADDRESS:
ADDRESSES: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
                                                                                                                                                                                                                                                  Query Match 9,9%; Score 152; DB 2; Length 288; Best Local Similarity 27.7%; Pred. No. 7.4e-06; Matches 48; Conservative 24; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.9%; Score 152; DB 2; Length 288; 27.7%; Pred. No. 7.4e-06; tive 24; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Derver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BE PC compatible
COMPUTER: BEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT ARPLICATION DATA:
APPLICATION NUMBER: US/08/976,838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIPICATION: 435
ATTORNEY, FAGENT INPORMATION:
NAME: Comnell, Gary J.
REGISTRATION NUMBER: 32,020
REPERBENCHOCCHEN NUMBER: 2848-11-C2
TELECOMMUNICATION INPORMATION:
TELEPAN: (303) 863-9700
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                          TELEPHONE: (303) 863-9700
TELEPAX: (303) 863-023
INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                               : 288 amino acids
amino acid
                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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Best Local Similarity
Matches 48; Conserv
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US-08-976-838-15
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                                                                                                                    LENGTH:
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35 PNVSQ-GCQG-GCATCSDYNGCLSCKPRLFFVLERIGMKQIGVCLSSCPSGYYGTRYPDI 92

48; Conservative

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93 NKCTKCKVDCDTCFNK--NPCTKCKSGFYLH--LGKCLDSCPEGLEANNHTMECVSIVHC 148
13 PECSEVGCOGPGPDHCND---CL---HYYYKLK----NNTRICVSSCPPGHY---HADK 58
                                                                                                                                                                              113 ------RKCSENPKTC----TEFHICTECRDGLSL----QGSRCSVSCE 147
                                                                                                                                                   149 EASEWSPWSPCMKKKKTCGFKRGTE----TRVRDILQHPSAKGKCNLCPPTSE 197
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Job time : 14.5595 secs
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US-09-894-912A-32
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Sequence 13, Appl
Sequence 16, Appl
Sequence 48, Appl
Sequence 25, Appl
Sequence 26, Appl
Sequence 16, Appl
Sequence 172, Appl
Sequence 174, Appl
Sequence 174, Appl
Sequence 174, Appl
                                                                                                                                June 29, 2004, 17:02:26; Search time 37.5837 Seconds (without alignments) 2098.641 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10,
Sequence 34,
Sequence 23,
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Sequence 166,
Sequence 48,
Sequence 25,
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                                                                                                                                                                                                                                                                                1 MHLRLISCPFIILNFMEYIG......QQKRRARDKQQKSVSVSTVH 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1: /cgr2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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10 US-09-894-912A-13

10 US-09-894-912A-14

10 US-09-894-912A-13

10 US-09-745-763-166

10 US-09-745-763-166

10 US-09-984-912A-26

10 US-09-894-912A-26

10 US-09-894-912A-16

10 US-09-894-912A-16

10 US-09-894-912A-16

10 US-09-894-912A-16

10 US-10-185-770-4

10 US-10-185-770-4

10 US-10-094-886-176

US-10-094-886-176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published_Applications_AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                        Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                               US-09-894-912A-32
1535
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Maximum DB seq length: 2000000000
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Match Length
                                                                                                                                                                                                                                                                                                                                  BLOSUM62
                                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
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21	632	41.2	265	14	US-10-125-852-24	
22	629	41.0	229	10	US-09-894-912A-25	
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24	571.5	37.2	243	14	US-10-185-770-2	
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56	569.5	37.1	243	16	US-10-467-042-12	
27	265	9	250	14	US-10-125-852-3	
28	536	34.9	222	14	US-10-125-852-15	Sequence 15, Appl
29	531.5	4	229	14	US-10-125-852-6	9
30	403.5	26.3	190	12	US-10-087-192-873	873
31	370.5	24.1	161	12	US-10-087-192-876	876
32	267	17.4	46	10	US-09-894-912A-18	18
33	241.5	15.7	131	14	US-10-125-852-9	6
34	208	13.6	110	14	US-10-125-852-11	H
35	193	12.6	37	10	US-09-894-912A-20	ñ
36	187	12.2	1548	13	US-10-180-903-2	Sequence 2, Appli
37	181.5	11.8	43	14	US-10-125-852-7	~
38	179	11.7	696	10	US-09-961-403-6	
39	170.5	11.1	942	15	US-10-369-493-5070	
40	150	9.6	42	10	US-09-894-912A-22	
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43	144.5	9.4	2471	15	US-10-369-072-27	
44	142.5	9.3	807	14	US-10-205-194-133	133,
45	140.5	9.5	9	12	US-09-939-853A-96	Sequence 96, Appl
					ALIGNMENTS	
RESULT	_					
US-09-8	US-09-894-912A-32	32				

GENERAL INVERNITOR:

APPLICANT: Tang et al.

TITLE OF INVERTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH

TITLE OF INVERTION: FACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVERTION: FACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVERTION: FACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES

CURRENT APPLICATION NUMBER: US/09/894,912A

CURRENT APPLICATION NUMBER: To be assigned

PRIOR APPLICATION NUMBER: 60/266,614

PRIOR PILING DATE: 2000-04-05

PRIOR PILING DATE: 2000-06-28

PRIOR PILING DATE: 2000-04-05

PRIOR PILING DATE: 2000-04-05

PRIOR PILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PACENTIN VERSION 3.0

SEQ ID NOS: 48

LENGH: 279 i-09-894-912A-32 Sequence 32, Application US/09894912A Publication No. US20030044792A1 GENERAL INFORMATION:

ORGANISM: Mus musculus

Gaps ö 100.0%; Score 1535; DB 10; Length 279; 100.0%; Pred. No. 1.2e-114; tive 0; Mismatches 0; Indels 0; Matches 279; Conservative Query Match Best Local Similarity

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9 MHLRLISCFFIILMFWBYIGSQNASRGRRQRRWHPNVSQGCQGGCATCSDYNGCLSCKPR 60 1 MHLRLISCPPIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR

61 LPPVLERIGMKQIGVCLSSCPSGYYGTRYPDINKCTXCKVDCDTCPNKNPCTKCKSGPYL 120

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Publication No. US20030044792A1
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                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tang et al.

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH:
TITLE OF INVENTION: PACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: PACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REPREBACE: 28110/37260A
CURRENT PILING DATE: 2002-05-10
PRIOR PILING DATE: 2001-04-05
PRIOR PILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR PLICATION NUMBER: 60/215,733
PRIOR PLICATION NUMBER: 09/757,562
PRIOR PLING DATE: 2001-01-09
PRIOR PLING DATE: 2001-01-09
PRIOR PLING DATE: 2001-04-05
PRIOR PLING DATE: 2001-04-05
PRIOR PLING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 48
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                                                                                                                                                   HLGKCLDSCPEGLEANNHTMECVSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDIL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 QHPSA--KGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGESKR--AIPDSK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MHERLISWLFIIINFWBYIGSQWASRGRRQRRMHPWVSQGCQGCATCSDYNGCLSCKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MHLRLISCPFIILNFWBYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.7%; Score 1315.5; DB 10; Length 272; 87.1%; Pred. No. 3.8e-97;
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                                                                                                                                                                                                    241 GLESSIETPDQQENKERQQQQKRRARDKQQKSVSTVH 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 3.8e-97;
11; Mismatches 18
                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/09894912A Publication No. US20030044792A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 87.1
Matches 243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                          RESULT 2
US-09-894-912A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-894-912A-10
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                     19
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; Sequence 34, Application US/09894912A

US-09-894-912A-34

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Sequence 23, Application US/10125852

Publication No. US20030032034A1

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

ITILE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH FACTOR-ITILE OF INVENTION: METHODS AND POLYNUCLEOTIDES

FILE REFERENCE: HYS-43A

CURRENT APPLICATION NUMBER: US/10/125,852

CURRENT FILING DATE: 2001-08-30

PRIOR PILING DATE: 2001-08-30

PRIOR PILING DATE: 2001-08-30

PRIOR PILING DATE: 2001-08-30

PRIOR PILING DATE: 2001-08-30

PRIOR FILING DATE: 2001-03-05

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin version 3.1

SEQ ID NO 23
APPLICANTION:
APPLICANTION:
APPLICANT: Tang et al.
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
APPLICANT: Tang et al.
TITLE OF INVENTION: METCOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 28110/37260A
CURRENT APPLICATION NUMBER: US/09/994,912A
CURRENT PILING DATE: 2002-05-10
PRIOR FILING DATE: 2001-02-05
PRIOR PLILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR PILING DATE: 2001-02-05
PRIOR PILING DATE: 2000-06-29
PRIOR PILING DATE: 2000-06-29
PRIOR PILING DATE: 2000-06-39
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
SPRIOR FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 34
LENGTH: 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 OHPSAKGKGNLCPPTSETRTCIVQRKKCSKGERGKKGRERKRKKLANKBERKETSSSSDSK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 QHPSA--KGNLCPPTNETRKCTVQRKKCQKGRRKKKRRKKKRNKGRSKE--AIPDSK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LPFALERIGHKOIGVCLSSCPSGYYGTRYPDINKCTKCKADCDFCFNKNPCTKCKSGFYL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 85.7%; Score 1315.5; DB 10; Length 272; Best Local Similarity 87.1%; Pred. No. 3.8e-97; Matches 243; Conservative 11; Mismatches 18; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-894-912A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
GRGANISM: Homo sapiens
US-10-125-852-23
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61 LPFVLERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKVDCDTCPNKNPCTKCKSGFYL 120
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183 HPSA--KGNLCPPTNETRKCTVQRKKCOKGERGKKGRERKRKKPNKGESKE--AIPDSKS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MHIRLISCPFIILNFWEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR
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9
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Treacy, Maurice
Spaulding, Vikk,
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTEY: U.S.A.

ID: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: BESTER: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/745,763

FILING DATE: 18-Jun-2000
CLASSIPICATION: CUNCHOMN-
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21; Indels
                                               242 LESSIETPDQQENKERQQQQKRARDKQQKSVSVSTVH 279
                                                               84.2%; Score 1293; DB 9;
85.1%; Pred. No. 2.6e-95;
iive 14; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 219
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 166:
US-09-745-763-166
                                                                                                                                                                                                Sequence 166, Application US/09745763
Sequence 166, Application US/09745763
Sequence No. US20020065394A1
GENERAL INPORMATION:
MCCOY, John M.
Lavalite, Edward R.
Collins-Racie, Lisa A.
Evans, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Sprunger, Suzanne A. REGISTRATION NUMBER: 41,323 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (617) 498-8284
TELERAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 166:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 292 amino acids
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TOPOLOGY: linear
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Matches 235; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Cambridge
                                                                                                                                                                                  US-09-745-763-166
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Publication No. US20030044792A1
GENERAL INFORMATION:
APPLICANT: Tang et al.
APPLICANT: TARGE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH
TITLE OF INVENTION: PACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES
PILE REFERENCE: 28110/37260A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 HLGKCLDNCPEGLRANNHTWECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII 180
                                                                                                                                                                                                                                                                                                                                                                                                                    PPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLH 122
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                                                                                                                                             1 MHLALISWLFIILNFWEYIGSQNASRGRRQRRWHPNVSQGCQGGCATCSDYNGCLSCKPR
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                                                                                                                   1 MHLRLISCFFIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGCCATCSDYNGCLSCKPR
                                                                      Gaps
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                       85.7%; Score 1315.5; DB 14; Length 272; 87.1%; Pred. No. 3.8e-97; tive 11; Mismatches 18; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 GLESSIETPDQQENKERQQQQKRRARDKQQKSVSVSTVH 279
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CURRENT PELICATION NUMBER: US/09/894,912A

CURRENT FILING DATE: 2002-05-10

PRIOR PILING DATE: 2001-04-05

PRIOR PILING DATE: 2001-04-05

PRIOR PILING DATE: 2001-04-05

PRIOR PILING DATE: 2001-02-05

PRIOR PILING DATE: 2001-02-05

PRIOR PILING DATE: 2001-01-09

SROFTWARE: Patentin version 3.0

SROTTWARE: Patentin version 3.0
                         Query Match 85.7% Best Local Similarity 87.1% Matches 243; Conservative
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Best Local Similarity 87.1%
Matches 242; Conservative
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Sequence 26, Application US/09894912A

Sequence 26, Application US/09894912A

Publication No. US20030044792A1

GENERAL INFORMATION:
APPLICANT: Tang et al.
TITLE OF INVENTION: PACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES
FILER REFERENCE: 28110/31260A

CURRENT APPLICATION NUMBER: US/09/894,912A

CURRENT PILING DATE: 2002-05-10

PRIOR APPLICATION NUMBER: 60/266,614

PRIOR PILING DATE: 2001-04-05

PRIOR PILING DATE: 2000-06-28

PRIOR PILING DATE: 2001-01-09

PRIOR PILING DATE: 2001-01-09

PRIOR PILING DATE: 2001-01-09

PRIOR PILING DATE: 2000-06-28

PRIOR PILING DATE: 2000-06-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 QHPSAKGKGNLCPPTSETRTCIVQRKKCSKGBRGKKGRERKRKKKKLNKBERKETSSSSDSK 240
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                                                                                                                                                                                                                                                                                                                                                                                     21; Indels
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                                                                                                                                                                                                                                                                                                                          Query Match 84.2%; Score 1293; DB 14; Best Local Similarity 85.1%; Pred. No. 2.6e-95; Matches 235; Conservative 14; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 GLESSIETPDQQENKERQQQQKRRARDKQQKSVSVS 276
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86.7%; Pred. No. 1e-94;
Live 12; Mismatches 18;
                                  09/799,451
PRIOR FILING DATE: 2001-08-30
PRIOR PRILING DATE: 2001-03-05
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
SEQ ID NO 25
LENGTH: 292
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Best Local Similarity 86.7%
Matches 234; Conservative
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US-10-125-852-25
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US-09-894-912A-26
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Publication No. US20030032034A1
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH FACTOR-I
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: H75-43A
CURRENT PILING DATE: 2002-08-20
CURRENT FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: US 60/316,368
                                                                                                                                                                                                                                         US-09-894-912A-48

Sequence 48, Application US/09894912A

Sequence 48, Application US/09894912A

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVERTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH

TITLE OF INVERTION: FACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 H.G.C.DICEBGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII 180
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      181 QHPSA--KGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGESKB--AIPDSK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MHLRLISWLFIILNFWEYIGSQNASRGRRQRRWHPNVSQGCQGGCATCSDYNGCLSCKPR 60
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                                                        241 GLESSIETPDOQENKERQQQQKRRARDKQQKSVSVS 276
                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: FACION-LIALS FULIFERINGS
FILE REFERENCE: 28110/37260A
CURRENT APPLICATION NUMBER: US/09/894,912A
CURRENT FILING DATE: 2002-05-10
FRIOR APPLICATION NUMBER: CO & 66,614
FRIOR FILING DATE: 2001-04-05
FRIOR APPLICATION NUMBER: 60/266,614
FRIOR APPLICATION NUMBER: 60/215,733
FRIOR APPLICATION NUMBER: 60/215,733
FRIOR APPLICATION NUMBER: 09/157,562
FRIOR PELING DATE: 2001-09
FRIOR FILING DATE: 2001-01-09
FRIOR FILING DATE: 2000-04-05
NUMBER: 09 SEQ ID NOS: 48
SOFTWARE: PALENTING DATE: 2000-04-05
NUMBER: 09 SEQ ID NOS: 48
SOFTWARE: PALENTING DATE: 2000-04-05
NUMBER: 09 SEQ ID NOS: 48
SOFTWARE: PALENTING DATE: 2000-04-05
NUMBER: 09 SEQ ID NOS: 48
SOFTWARE: PALENTING DATE: 2000-04-05
NUMBER: 09 SEQ ID NOS: 48
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US-09-894-912A-48
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US-10-125-852-25
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; Sequence 4, Application US/10185770;
; Publication No. US2003002217A1
; GENERAL INFORMATION:
; APPLICANT: CECCARDI, Toni et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: USES THEREOF
; TITLE OF INVENTION: USES TO 10-0-02
; REIOR FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PASESEQ FOR WINGOWS VERSION 4.0
; SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 LPFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MHLRLISCPFIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 77.3%; Score 1187; DB 14; Length Best Local Similarity 92.5%; Pred. No. 5.7e-87; Matches 210; Conservative 5; Mismatches 10; Indels
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1782
LENGTH: 239
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90.1%;
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Best Local Similarity 90.1:
Matches 201; Conservative
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US-10-185-770-4
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US-10-087-192-1782
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Best Local Similarity
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US-10-087-192-1782
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                                                 61 LFFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNPCTKCKSGFYL 120
                                                                                                                                                            LFFVLERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKVDCDTCFNKNFCTKCKSGFYL 120
                                                                                                                               HLGKCLDSCPEGLEANNHTMECVSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDIL 180
                                                                                                                                                                                                                                             QHPSAKGKGKILCPPTSETRTC1VQRKKCSKGERGKKGRERKRKKLNKEERKETSSSSDSK 240
                                                                                                                                                                                                                                                                          181 QHPSA--KGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKKPNKGESKE--AIPDSK 236
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APPLICANT: Tang et al.

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL

TITLE OF INVENTION: PACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES

FILE REPERENCE: 28110/37260A

CURRENT APPLICATION NUMBER: US/09/894,912A

CURRENT PILING DATE: 2002-05-10

FRIOR APPLICATION NUMBER: FO/266,614

PRIOR APPLICATION NUMBER: 60/266,614

PRIOR APPLICATION NUMBER: 60/215,733

PRIOR PILING DATE: 2001-02-05

FRIOR APPLICATION NUMBER: 09/757,562

PRIOR APPLICATION NUMBER: 09/757,562

PRIOR APPLICATION NUMBER: 09/543,774

PRIOR PILING DATE: 2001-01-09

FRIOR APPLICATION NUMBER: 09/543,774

PRIOR FILING DATE: 2001-04-05

NUMBER: OF SEQ ID NOS: 48

SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NO 16

1 DATE: 2010 NO 16
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                                                                                                                                                                                                                                                                                                                                                        241 GLESSIETPDQQENKERQQQQKRRARDKQQ 270
                                                                                                                                                                                                                                                                                                                                                                                     237 SLESSKRIPEQRENK--QQQKKRKVQDKQK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 16, Application US/09894912A; Publication No. US20030044792A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-10-185-770-4
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Length 225;

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Pred. No. 8.6e-83;
6; Mismatches 14; Indels 2
                                                                                                   QHPSAKGKGNLCPPTSETRTCIVQRKKCSKGERGKKGRERKRKKLNK 227
                                                                                                                                                                                                                                          Sequence 1782.

Publication No. US20020182586A1

GENERAL INFORMATION:

APPLICANT: Morris, David W.

APPLICANT: Engelhard, Eric K.

TITLE OF INVENTION: NOVEL CCMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: NOVEL CCMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: 000 CCMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: 000 CCMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: 000 CCMPOSITIONS AND METHODS FOR

FILE OF INVENTION NUMBER: US/10/087,192

CURRENT APPLICATION NUMBER: US 09/747,377

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US 09/798,586
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117 GFYLHLGKCLDSCPRCLEANNHTMECVSIVHCEASEWSPWSPOWKKGKTCGFKRGTETRV 176
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                                                                                                                                                           Gaps
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9
                                                                                                                          Length 239;
                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                 177 RDILQHPSAKGKGNLCPPTSBTRTCIVQRKKCSKGERG 214
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90.4%; Score 1100; DB 15;
Best Local Similarity 90.4%; Pred. No. 5.4e-80;
Matches 197; Conservative 5; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/313,182
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/288,052
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Padigaru, Muralidhara
Taupier, Raymond J., Jr.
Miller, Charles
Casman, Stacie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shimkets, Richard
Rastelli, Luca
Spaderna, Steven
LaRochelle, William
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Malyankar, Uriel M.
Boldog, Ferenc
Guo, Xiaojia
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Burgess, Catherine
Vernet, Corine A.
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APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiachong
APPLICANT: Spyrek, Kimberly A.
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Gusev, Vladimir
Smithson, Glennda
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Gerlach, Valerie
Pochart, Pascal
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NUMBER OF SEQ ID NOS: 298
SOFTWARE: Patentin 2.1
SEQ ID NO 172
LENGTH: 239
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pena, Carol
                                                                                ORGANISM: Homo sapiens
US-10-094-886-172
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US-10-094-886-176
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TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOR
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOR
PILE REPERENCE: 21402-290 B
CURRENT PELICATION NUMBER: US/10/094,886
CURRENT FILING DATE: 2002-03-07
                                                                              HIGKCLDSCPEGLERNNHTWECVSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDIL 180
              LPPVLERIGHKOIGVCLSSCPSGYYGTRYPDINKCTKCKVDCDTGFNKNPCTKCKSGPYL 120
                                                                                                   Prior Application data removed - See File Wrapper or PALM.
                                                                                                                                                                      181 OHPSAKGKGNLCPPTSETRTCIVORKKCSKGERGKKGRERKRK 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURKEAN TILLING DATE: CULT-CU-7, TOURIGEN FILLING DATE: 2001-03-08 PRIOR PELICATION NUMBER: 60/214, 332 PRIOR FILLING DATE: 2001-03-08 PRIOR FILLING DATE: 2001-08-17 PRIOR FILLING DATE: 2001-05-05 PRIOR PELICATION NUMBER: 60/218, 510 PRIOR PELICATION NUMBER: 60/318, 510 PRIOR PELICATION NUMBER: 60/318, 510 PRIOR PELICATION NUMBER: 60/214, 281 PRIOR PELICATION NUMBER: 60/214, 194 PRIOR PELICATION NUMBER: 60/274, 849 PRIOR PELING DATE: 2001-03-09 PRIOR PELING DATE: 2001-08-21 PRIOR PELING DATE: 2001-08-21
                                                                                                                                                                                                                                                                        Sequence 172, Application US/10094886 Publication No. US20040002120A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shenoy, Suresh
Padigaru, Muralidhara
Taupier, Raymond J., Jr.
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Liu, Xiaohong
Spytek, Kimberly A.
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Malyankar, Uriel M.
Boldog, Ferenc
Guo, Xiaojia
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Gangolli, Esha
Gusev, Vladimir
Smithson, Glennda
Zerhusen, Bryan
Gerlach, Valerie
Pochart, Pascal
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Burgess, Catherine
Vernet, Corine A.
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Rastelli, Luca
Spaderna, Steven
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Casman, Stacie
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                                                                                                                                                                                                                                                      RESULT 13
US-10-094-886-172
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US-10-094-886-174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GSQNASRGRRQRRMFPNVSQGCQGGCATCSDYNGCLSCKPRLFFALFRIGMKQIGVCLSS 60
                                PRIOR FILING DATE: 2001-09-00

PRIOR FILING DATE: 2001-09-00

PRIOR FILING DATE: 2001-03-08

PRIOR FILING DATE: 2001-03-08

PRIOR FILING DATE: 2001-03-08

PRIOR FILING DATE: 2001-03-08

PRIOR FILING DATE: 2001-03-09

PRIOR FILING DATE: 2001-03-09

PRIOR PLING DATE: 2001-06-01

PRIOR PLING DATE: 2001-06-01

PRIOR PLING DATE: 2001-06-01

PRIOR PLING DATE: 2001-06-21

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 298

SEQ ID NO 176

LENGTH: 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 GSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRLPFVLERIGMKQIGVCLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 92.8%; Pred. No. 1.1e-75; Matches 181; Conservative 5; Mismarched
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Gorman, Linda
Malyankar, Uriel M.
Boldog, Ferenc
Guo, Xiaojia
Shenoy, Sureah
Padigaru, Muralidhara
Taupier, Raymond J., Jr.
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Publication No. US20040002120A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Tchernev, Velizar T.
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A.
                         PPLICATION NUMBER: 60/318,510
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Burgess, Catherine
Vernet, Corine A.
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Gangolli, Esha
Gusev, Vladimir
Smithson, Glennda
Zerhusen, Bryan
Gerlach, Valerie
FILING DATE: 2001-05-02
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Casman, Stacie
                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-886-176
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APPLICANT: LANCORDELE, WALLIAGUM
APPLICANT: LANDING, Mei
ITILE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
IFILE REFERENCE: 21402-290
ITILE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
IFILE REFERENCE: 21402-290
ICHRENT APPLICATION NUMBER: 00/204,322
PRIOR PLILNG DATE: 2001-00-17
PRIOR PLILNG DATE: 2001-00-17
PRIOR PLILNG DATE: 2001-00-17
PRIOR PLILNG DATE: 2001-00-10
PRIOR PLILNG DATE: 2001-00-10
PRIOR PLILNG DATE: 2001-00-20
PRIOR PLILNG DATE: 2001-00-20
PRIOR PLILNG DATE: 2001-00-21
PRIOR PLILNG DATE: 2001-00-20
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PRIOR PLING DATE: 2001-00-20
PRIOR PLING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: June 29, 2004, 17:15:57 Job time : 37.5837 secs
                                                                                                Rastelli, Luca
Spaderna, Steven
LaRochelle, William
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Pernandes, Elma
Shimkets, Richard
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 29, 2004, 16:56:05; Search time 14.2209 Seconds (without alignments) 1887.186 Million cell updates/sec

US-09-894-912A-32 1535 1 MHLRLISCFFIILNFMEYIG......QQKRRARDKQQKSVSVSTVH 279 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched: 283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	serine proteinase	furin (BC 3.4.21.7	subtilisin-like pr	subtilisin-like pr	subtilisin-11ke pr	furin (BC 3.4.21.7	_	protein bli-4D [im	probable proprotei	subtilisin-like pr	probable kexin (EC	gene PACB4 protein	subtilisin-like pr	subtilisin-like pr	insulin-like growt		cell-fate determin	F-spondin - rat	Motch B protein -	Wnt inhibitory fac	insulin-like growt	Xotch protein - Af	Wnt inhibitory fac	hypothetical prote	hypothetical prote	protein-tyrosine k			insulin receptor (
SUMMARIES	OI.	534583	T43251	A39490	JC5571	JC5570	A43434	152527	D87803	B48225	A48225	T37314	153282	G02428	JC6148	A33837	A47723	A49128	A38152	A49175	B59180	IGHUR1	A35844	A59180	T24232	T27283	S70713	B47417	B36502	S57245
	DB	7	7	-	7	7	7	~	~	~	-	~	7	~	N	N	~	~	7	~	7	-	~	~	7	~	~	N	N	0
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	Query Match	12.2	12.1	11.7	11.4	11.4	11.3	11.1	11.1	10.7	10.7	10.6	10.5	10.0	10.0	9.7	9.5	9.4	9.3	9.5	9.1	9.1	9.1	9.0	8.9	e. B	8.9	•	8.5	8.5
	Score	187	185.5	179	174.5	174.5	174	171	170.5	164	163.5	162	161	154	154	149	145.5	144.5	142.5	140.5	140	139.5	139	138.5	137	137	136.5	133	131	131
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ingulin receptor	ingulin receptor p	notch protein nomo	notch-1 protein -	ingulin receptor p	insulin receptor p	transmembrane prot	notch protein homo	hypothetical prote	tumor necrosis fac	furin (BC 3.4.21.7	trophozoite cystei	cysteine rich prot	trophozoite surfac	insulin receptor-r	probable transform
A56081	INHUR	S18188	A46019	A34157	A36080	S42612	A40043	T26972	JC4302	S43656	C42125	T42017	A48579	A36502	826059
П	-	~	~	~	N	7	N	~	N	~	~	~	~	~	7
2148	1382	2531	2531	1372	1383	2437	2555	1111	461	837	677	1274	667	1300	375
8.5	S	9.S	8.5	8.4	8.4	8.4	8.4	9.4	8.3	8.5	8.2	8.2	8.1	8.1	8.0
131	130.5	130	130	129.5	129.5	129	129	128.5	128	126.5	126	125.5	124.5	124	123.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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serine C;Speci C;Date;	Serine proceinade (EC 3.4.71) Floa - Mouse C.Species: Mus musculus (house mouse) C.Date: 02-Dec-1993 #sequence revision 10-Nov-1995 #text change 05-Nov-1999
C, Acces	С. Accession: S34583 R. Nakaqawa, Т.; Murakami, К.; Nakayama, К.
FEBS Le	FEBS Lett. 327, 165-171, 1993 A.Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a
A; Refer	A;Reference number: \$34583; MUID:93327934; PMID:8335106
A;Stati	Afficers. Descriptions Afficient Afficients for the Afficient Affi
A;Resic A;Cross	A; Residues: 1-1548 < NAK> A; Cross_references: GB: D17583; NID: 9407344; PIDN: BAA04507.1; PID: d1005033; PID: 9440374
in Fame day	
Query Ma Best Lo	Query Match Query Match 27.8%; Pred. No. 0.0001; Matches 52; Conservative 21; Mismatches 72; Indels 42; Gaps 11; Matches 52; Conservative 21; Mismatches 72; Indels 42; Gaps 11;
È	38 SQGQQGGATCSDYNGCLSCKPRLFFVLERIGMKQIGVCLSSCPSGYYGTRYPDIN 93
qa	880 NOPCHSSCXTCNGSLCASCPTGMYLMLQACVPSCPGGTWPSVTSG 924
è	94 KCTKCKVDCDTCPNKNPCTKCKSGPYLHLGKCLDSCPEGLEANNHTWECVSIVHCE 149
g	925 SCEKCSEDCVSCSGADLCQQCLSQPDNTLLLHEGRCYHSCPEGFYAKDGVCEHCS 979
È	150 ASEWSPWSPCMKKGKTCGPKRGTETRVRDILQHPSAKGKGNLCPPTSETRTCIV 203
Dp	980SPCKTCEGNATSCNSCEGDFVLDHGVCWKTCPEKHVAVEGVCKHCPERCQDCIH 1033
ò	204 QRKKC 208
£	1034 BKTCKBC 1040

RESULT 2
T43251
furin (EC 3.4.21.75) - fall armyworm
Kurin (EC 3.4.21.75) - fall armyworm
Klurin (EC 3.4.21.75) - fall armyworm
Klurin (EC 3.4.21.75) - fall armyworm
C; Species: Spodoptera frugiperda (fall armyworm)
C; Species: Spodoptera frugiperda (fall armyworm)
C; Species: Spodoptera frugiperda (fall armyworm)
C; Accession: T43251
R; Cieplik, M.; Klenk, H.
submitted to the EMBL Data Library, January 1996
A; Reference number: Z22368
A; Reference number: Z22368
A; Reference number: Z22368
A; Recession: T43251
A; Reference prediminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA

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subtilisin-like proprotein convertage (BC 3.4.21.-) PACE4 precursor, splice form E-II - C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C; Accession: JC5571
R; Mori, K.; Kii, S.; Tsuji, A.; Nagahama, M.; Imamaki, A.; Hayashi, K.; Akamatsu, T.; Ni A; Hicker, 121, 941-948, 1997
A; Title: A novel human PACE4 isoform, PACE4E is an active processing protease containing A; Reference number: JC5570; MUID:97335942; PMID:9192737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Experimental source: brain cerebellum C;Comment: This enzyme is a processing protease and responsible for processing of varion ch it is retained intracellularly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cjaccession: JG5570
RjMori, K.; Kii, S.; Tsuji, A.; Nagahama, M.; Imamaki, A.; Hayashi, K.; Akamatsu, T.; Ni Blochem. 121, 941-948, 1997
A;Title: A novel human PACR4 isoform, PACR4E is an active processing protease containing A;Reference number: JC5570; MUID:97335942; PMID:9192737
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C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YPGDTAARRCRR------CHKGCRTCSSRAATQCLSCR-RGFY-----HHQEMAT 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----PWSP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           825 PDSBLIRCGECHHTCGTCVGPGREECIHCAKNFHFHDWKCVPACGEGFYPREMPGLPHKV 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Cross-references: DDBJ:D87994; NID:g2330550; PIDN:BAA21792.1; PID:g2330551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: DDBJ: D87993; NID: 92330548; PIDN: BAA21791.1; PID: 92330549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 CLSSCPSGYYGTRYPDINKCTKCVDCDTCPNK-NPCTKCKSGFYLHLGKCLDSCPEGLB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 YIGSQNASRGRRORRMHPNVSQGCQGGCATCSD--YNGCLSCKPRLFFVLERIGMKQIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Map position: 15q26-15q26
C;Superfamily: subtilisin-like proteinase PACB4; subtilisin homology
C;Superfamily: subtilisin-like proteinase proteinase
C;Keywords: glycoprotein; hydrolase; serine proteinase
F;1-G2/Domain: signal sequence #status predicted <PRO>
F;196-434/Domain: propeptide #status predicted <PRO>
F;196-434/Domain: subtilisin homology <PRO>
F;306-544/Domain: hydrophobic cluster #status predicted <PGL>
F;306-546,347,420/Active site: Asp, His, Asm, Ser #status predicted
F;205,246,347,420/Active site: Asp, His, Asm, Ser #status predicted
F;259/Binding site: carbohydrate (Asm) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----VSIVHCEAS----EWS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 CMKKGKTCGPKRGTETRV-----RDILQHPSAKGKGNLCPPT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRRYGPPGGEROATVSSKGVPGGQSLSASSPGAGEGMLHHPT 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.4%; Score 174.5; DB 2
23.9%; Pred. No. 0.00045;
tive 25; Mismatches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GDB:131390; OMIM:167405
                                                                                                                                                                                                                                                                                                                                                                                              A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-962 <MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 ANNHTMBC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-975 < MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: JC5570
                                                                                                                                                                                                                                                                                                                                                               A; Accession: JC5571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: GDB: PACE4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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A; Residues: 1-1299 <CIE>
A; Cross-references: EMBL: 268888; NID: g1167859; PID: e219690; PIDN: CAA93116.1
A; Experimental source: clone Sfurin 6; ovary
C; Function:
A; Description: responsible for the endoproteolytic processing of proproteins with specif C; Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form A - hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.Alternate names: kexin homolog
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Mar-2000
C;Accession: A39490
R;Kiefer, M.C.; Tucker, J.B.; Joh, R.; Landsberg, K.B.; Saltman, D.; Barr, P.J.
DNA Cell Biol. 10, 757-769, 1991
A;Title: Identification of a second human subtilisin-like protease gene in the fes/fps
A;Reference number: A39490; MUID:92075167; PMID:1741956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142
                                                                                                                                                                                                                                                                                                                                                                                                     -----VSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLSSCPSGYYGTRYPDINKCTKCKVDCDTCPNK-NPCTKCKSGPYLHLGKCLDSCPEGLE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 ANNHTMEC------PWSP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CMKKGKTC----GFKRG-----TETRVRDILQHPSAKGKGNLCPPTSETRTCIVQRK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        898 CRRCDENCLSCAGSSRNCSRCKTGFTQLGTSCITNHTCSNADETPCEMVKSNRLC--ERK 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 PDSELIRCGECHHTCGTCVGPGREECIHCAKNFHFHDWKCVPACGEGFYPEEMPGLPHKV 897
                                                                                                                                                                                                                                                                                                                                                                  94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 YIGSQNASRGRRQRRMHPNVSQGCQGGCATCSD--YNGCLSCKPRLPFVLERIGMKQIGV 75
                                                                                                                                                                                                                                                                                                                                                                  36 NVSQGCQGGCATCSD-YNGCLSCKPRLFFVLERIGMXQIGVCLSSCPSGYYGTRYPDINK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Mesidues: 1-969 < KIE>
A; Cross-references: GB: M80482; NID: g189531; PIDN: AAA59998.1; PID: g189532
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           904 TSAFCLSCEPKWELNKKGKCMPVGSDKCSAGEFAVDQKCKRCNPACDSCYGEN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 15q26-15q26
C;Superfamily: subtilisin-like proteinase PACB4; subtilisin homology
                                                                                                                                                                                                                                                                                                 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTKCKVDCDTCP--NKNPCTKCKSGPYLHLGKCLDSCPEGLEANNHTMEC----
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                                                                                                                                                                                                                                   DB 2; Length 1299;
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$150-969/Product: serine proteinase PACB# #status predicted <SIG>
P;196-434/Domain: subtilisin homology <SBT>
P;205,246,420/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.7%; Score 179; DB 1; Length 969; 23.3%; Pred. No. 0.00023; Live 23; Mismatches 89; Indels
                                                                                                                                                                                                                               ch 12.1%; Score 185.5; DB 2; Length 1
1 Similarity 24.5%; Pred. No. 0.00011;
54; Conservative 24; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 QHPSAKGKGNLCPPTS -- ETRTCIVQRKKCSKGERGKKGR 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: GDB:PACE4
A;Cross-references: GDB:131390; OMIM:167405
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                                                                                                                                                                                                                               Query Match
Best Local Similarity
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Directin bli-4D [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 21-Jun-2002
C;Accession: D87803
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Reference number: A75000; MUID: 99065813; PMID: 9951916
A;Reference number: appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                          C;Accession: 152527 ... Nakayama, K. R;Hosaka, M.; Murakami, K.; Nakayama, K. Biomed. Res. 15, 383-390, 1994 ... Aprille: PACE4A is a ubiquitous endoprotease that has similar but not identical substrat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CMKKGKTC----GPKRG-----TETRVRDILQHPSAKGKGNLCPPTSETRTCIVQRK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    861 CRRCEENCLSCEGSSRNCSRCKAGFTQLGTSCITNHTCSNADETFCEMVKSNRLC--ERK 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    674 NCHDECNGCTESSSATSCPACK-HLTQTLRNKGGSGP-KCVQKCDDTY----YLDGDKC 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75
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                                                                                                                                                                                  PACB4A - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 YIGSQNASRGRRORRMHPNVSQGCQGCATCSDYN--GCLSCKPRLFFVLERIGMKQIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               700 YFGDAAARRCRR------HHQETCTGRSPAQCLSCR-RGFY-----HHQETNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 CLSSCPSGYYGTRYPDINKCTKCKVDCDTCPNK-NPCTKCKSGPYLHLGKCLDSCPBGLB
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 NVSQCCQCCATCSDYNGCLSCKPRLPFVLERIGMKQIGVCLSSCPSGYYGTRYPDINKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-932 <RES>
A;Cross-references: GE:D50060; NID:g769700; PIDN:BAA08777.1; PID:g769701
C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
F;172-410/Domain: subtilisin homology <SET>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.1%; Score 171; DB 2; Length 932; 22.9%; Pred. No. 0.00073; tive 25; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.1%; Score 170.5; DB 2; Length : 28.3%; Pred. No. 0.0008; tive 18; Mismatches 75; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: 152527
A;Accession: 152527
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                --- PCOEGCKTC 1170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 22.99
Matches 55; Conservative
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A;Molecule type: DNA
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                                1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 furin (BC 3.4.21.75) 2 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Mar-2000
C;Accesion: A4434
R;Roebroek, A.J; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, B. Biol. Chem. 267, 17209-17215, 1992
A;Title: Cloning and functional expression of Dfurin2, a subtilisin-like proprotein prodA;Reference number: A4334; MUID:92381036; PMID:1512259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 NKCTKCKVDCDTCF--NKNFCTKCKSGFYLHLGKCLDSCPEGLEANNHTMECVSIVHCEA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 CLSSCPSGYYGTRYPDINKCTKCKVDCDTCFNK-NFCFKCKSGFYLHLGKCLDSCPEGLE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 ANNHTMEC------PSIVHCEAS----EWS-----PWSP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    838 PDSELIRCGECHHTCGTCVGPGREECIHCAKNFHFHDWKCVPACGEGFYPERMPGLPHKV 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75
                      A.Map position: 15q26-15q26
C;Superfamily: subtilisin-like proteinase PACB4; subtilisin homology
C;Reyrords: alternative splicing; glycoprotein; hydrolase; serine proteinase
F;1-62/Domain: signal sequence #status predicted <SIG>
F;63-149/Domain: propeptide #status predicted <PRO>
F;95-964/Domain: pubtilisin homology <SBT>
F;95-964/Domain: hydropholic cluster #status predicted <HCL>
F;25-964/Domain: hydropholic cluster #status predicted
F;25-964/Domain: propeptide #status predicted
F;259/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 YIGSQNASRGRRQRRMHPNVSQGCQGGCATCSD--YNGCLSCKPRLPFVLERIGMKQIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 NASRGRRQRRMHPN---VSQGCQGGCATCSDY--NGCLSCKPRLFFVLERIGMKQIGVCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A;Residues: 1-1680 <ROE>
A;Cross-references: GB:M94375; NID:g157461; PID:g157462
A;Note: sequence extracted from NCBI backbone (NCBIN:111933, NCBIP:111934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72; Gaps
                                                                                                                                                                                                                                                                                                                                              DB 2; Length 975;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: FlyBase:FBgn0004598
C;Superfamily: subtilisin homology
C;Keywords: hydrolase; serine proteinase; transmembrane protein
F;409-652/Pomain: subtilisin homology <SBT>
F;418,457,638/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                        81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 CMKKGKTCGFKRGTETRV-----RDILQHPSAKGKGNLCPPT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 11.4%; Score 174.5; DB 2
Best Local Similarity 23:9%; Pred. No. 0.00045;
Matches 53; Conservative 25; Mismatches 81
Cross-references: GDB:131390; OMIM:167405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 SSCPSGYY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A43434
A; Status: preliminary
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440 SCETCTAPGPMSCEKCSKG 458
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Best Local Similarity
Matches 54; Conserv
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A; Residues: 1-570 <THA>
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780 NGH--DC-
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Proc. Natl. Acad. Sci. U.S.A. 90, 6691-6695, 1993
A;Title: cDNA structure of the mouse and rat subtilisin/kexin-like PCS: a candidate prop
A;Reference number: A48225; MUID:93342056; PMID:8341687
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C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: A48225; JX0248
R;Lusson, J.; Vieau, D.; Hamelin, J.; Day, R.; Chretien, M.; Seidah, N.G.
R;Lusson, J.; Vieau, D.; Hamelin, J.; Day, R.; Chretien, M.; Seidah, N.G.
A;Title: CDNA structure of the mouse and rat subtilisin/kexin-like PC5: a candidate prop
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-915 4.145932; NID:g293327; PIDN:AAA74636.1; PID:g293328
A;Crose-references: GB:L14932; NID:g293327; PIDN:AAA74636.1; PID:g293328
B;Nakagawa, T.; Hosaka, M.; Torii, S.; Watanabe, T.; Murakami, K.; Nakayama, K.
J; Blochem: 113, 132-135, 1993
A;Title: Identification and functional expression of a new member of the mammalian Kex2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                **Reywords: duplication; glycoprotein; hydrolase; integrin binding; serine proteinase; 1.34/Domain: signal sequence #status predicted <SIG>; 1.34/Domain: signal sequence #status predicted <SIG>; 1.35-915/Product: probable proproption convertase 5 #status predicted <PRO>; 1.17-915/Product: probable proprotein convertase 5 #status experimental <MAT>; 1.17-915/Product: subtilisin homology <SET>; 1.37-915/Product = Nation homology <SET>; 1.37-314,388/Active site: Asp, His, Ser #status predicted
                               683 ADKKRCRKCAPNCESCFGSHADQCLSCRYGYFLNRETSSCVAQCPEGSYQDIKKNIC--- 739
96 TKCKVDCDTCFNKNPCTKCKSGFYL-----HL--GKCLDSCPEGLEANNHTMECVSIV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             640 PECSEVGCDGPGPDHCTDCLHYHYKLKNNTR-----ICVSSCPPGHF---H 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 PDINKCTKCKVDCDTCPNKNP--CTKCKSGPYLH--LGKCLDSCPEGLEANNHTMECVSI 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: PCS precursor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 23-Feb-1997
C;Accession: B48225
                                                                                                                   147 HCBASEWSPWSPCMKKGKTCGFKRGTETRVRDILLQHPSAKGKGNLCPPTSETRTC--IVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 PNVSQ-GCQG----GCATCSDYNGCLSCKPRLFFVLERIGMKQIGVCLSSCPSGYYGTRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 VHCEASEWSPWSPCMKKGKTC-GFKRGTETRVRDILQHPSAKGKGNLCPPTSE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Rosidues: 1-915 -4103-
A;Cross-references: GB:L14933
C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                              probable proprotein convertase (EC 3.4.21.-) 5 precursor - rat
                                                                                                                                                                                                                                       205 RKKCSKG 211
                                                                                                                                                                                                                                                                                               824 CEKCSKG 830
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C;Accession: T37314
R;Thacker, C.; Peters, K.; Srayko, M.; Rose, A.M.
R;Thacker, C.; Peters, K.; Srayko, M.; Rose, A.M.
B;Thacker, C.; Peters, K.;
A;Title: Jocus of Caenorhabditis elegans encodes structurally distinct kex2/sn
A;Tele: A;Reference number: Z21679; MUID:95293228; PMID:7774813
A;Accession: T37314
                                                                A Molecule type: mRNA

A; Residues: 1-915 < NAKA.

A; Residues: 1-915 < NAKA.

A; Cross-references: DBA:D12619; NID:g220565; PIDN:BAA02143.1; PID:g220566

A; Note: the authors translated the codon GGC for residue 915 as Ala

C; Superfamily: subtilisin-like proteinase PACR4; subtilisin homology

C; Superfamily: subtilisin-like proteinase PACR4; subtilisin homology

C; Reywords: duplication; glycoprotein; hydrolase; integrin binding; serine proteinase

F; 1-34/Domain: signal sequence #status predicted < PRO>

F; 1-15-915/Product: propeptide #status predicted < PRO>

F; 117-915/Product: proprotein convertesse PCS #status experimental < MAT>

F; 164-402/Domain: subtilisin homology < SBT:

F; 164-402/Domain: subtilisin homology < SBT:

F; 123, 214, 388/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 SSCPSGYYGTRYPDINK -- CTKCKVDCDTCPNKNFCTKCKSGFYLHLGKCLDSCPRGLEA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348 Y----YLDGDKCKOKCSSHCHTCTKAEVCETCPGSLLLIDVDNMPHYDHGKCVESCPPGLV 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : : | | : : | | : : ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 ANNHIMBCVSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDILQHPSAKGKGNLCPP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable kexin (EC 3.4.21.61) - Caenorhabditis elegans (fragment)
NiAlternate names: blisterase 4
NiAlternate names: blisterase 4
Cispecies: Caenorhabditis elegans
Cipecies: Caecorhabditis elegans
Cipate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 RRWHPNVSQG------CQGGCATCSDYNGCLSCKPRLFFVLERIGMKQIGVCLSSCPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 GSQNASRGRRQRRMHPNVSQGCQGCATCSDYNG--CLSCKPRLFPVLERIGMKQIGVCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 10.7%; Score 163.5; DB 1, Length 915; Best Local Similarity 29.1%; Pred. No. 0.0022; Matches 44; Conservative 18; Mismatches 50; Indels 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 570;
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C;Keywords: alternative splicing; hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
A;Reference number: JX0248; MUID:93224489; PMID:8468318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 10.6%; Score 162; DB 2; Similarity 27.1%; Pred. No. 0.0019; 54; Conservative 21; Mismatches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 NNHTMECVSIVHCRASEWSPWSPCMKKGKTC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----OPCHRPCATC 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 TSETRIC--IVQRKKCSKG 211
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Subtilisin-like proprotein convertase (EC 3.4.21.-) homolog - human N;Alternate names: PGA protease (EC 3.4.21.-) homolog - human C;Species: Homo sapiens (man) (pate: Homo sapiens (man) (pate: Homo sapiens (man) (pate: L) 40.6148 (man) (pate: L) 40.6148 (man) (pate: L) 7. Feducates; S.; Duke, R.; Franzusoff, A. Proc. Natl. Acad. Sci. U.S.A. 93, 7695-7700, 1996 (pate: Man) (pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     insulin-like growth factor I receptor precursor - rat
NiContains: insulin-like growth factor I alpha chain; insulin-like growth factor I beta of
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Aartus norvegicus (Norway rat)
Cispecies: Rattus norvegicus
Cispecies: Rattus norvegicus
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A;Residues: 1-364 KMR2.
A;Cross-references: GB:M27293
R;Kurachi, H.; Jobo, K.; Ohta, M.; Kawasaki, T.; Itoh, N.
R;Kurachi, H.; Jobo, K.; Comun. 187, 934-339, 1992
Biochem. Blopbya: Rea: Comun. 187, 934-339, 1992
A;Title: A new member of the insulin receptor family, insulin receptor related receptor,
A;Reference number: PC1130; MUID:92412145; PMID:1530648
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A;Residues: 1.1371 <PRD>
K;Werner, H.; Woloschak, M.; Adamo, M.; Shen-Orr, Z.; Roberts Jr., C.T.; LeRoith, D.
Proc. Natl. Acad. Sci. U.S.A. 86, 7451-7455, 1989
A;Title: Developmental regulation of the rat insulin-like growth factor I receptor gene.
A;Reference number: A33837; MUID:90017496; PMID:2477843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-915 <MIR>
A;Cross-references: GB:U56387; NID:g1498312; PIDN:AAC50643.1; PID:g1498313
C;Comment: This protein functions as a soluble enzyme within the secretory pathway. It
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C;Superfamily: subtilisin-like proteinase PACB4; subtilisin homology
C;Keywords: glycoprotein; hydrolase; serine proteinase
P;164-402/Domain: subtilisin homology <SBT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42;
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                                                           149 RASEWSPWSPCMKKGKTC-GFKRGTETRVRDILQHPSAKGKGNLCPPTSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 915;
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A;Accession: JC2461
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                                                                                                                                                                                                                                                            RESULT 14
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                                                                                                                                                                                                                                                       C;Accession: I53282
R;Johnson, R.C; Darlington, D.N.; Hand, T.A.; Bloomquist, B.T.; Mains, R.E.
Endocrinology 135, 1178-1185, 1994
A;Title: PACE4: a subtliisin-like endoprotease prevalent in the anterior pituitary and A;Reference number: I53282; MUID:94349873; PMID:8070361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EC 3.4.21.-) 5 precursor - human (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 CLSSCPSGYYGTRYPDINKCTKCKVDCDTCFNK-NPCTKCKSGPYLHLGKCLDSCPEGLE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----PWSP 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            866 CRRCDENCLSCEGSSRNCSRCKAGFTQLGTSCITNHTCSNADETFCEMVKSNRLC--ERK 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               624 PRCSEVGCDGPGPDHCND---CL----HYYYKLK----NNTRICVSSCPPGHY---HADK 669
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subtilisin-like proprotein convertase (BC 3.4.21.-) 5 precursor - human (fra
C;Species: Homo sapiens (man)
C;Species: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Mar-2000
                                                                                                                                                                 ;Species: Rattus norvegicus (Norway rat)
;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 YIGSONASRGRRORRMHPNVSQGCQGCCATCSDYN--GCLSCKPRLFFVLERIGMKQIGV
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A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-937 <RES>
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A;Accession: G02428
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-899 <REU>
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R,Reudelhuber, T.L.
submitted to the EMBL Data Library, Pebruary 1996
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Matches 54
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A; Molecule type: mRNA

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A.Residues: 913-984, 'PV', 987-1017 < KUR>
A.Cross-references: GB:D12679; NID:g220918; PIDN:BAA20983.1; PID:g4433359
A.Cross-references: GB:D12679; NID:g220918; PIDN:BAA20983.1; PID:g4433359
C.Superfamily: insulin receptor; protein kinase-related transforming protein; transmembr F;1-30/Domain: signal sequence #status predicted <SIG>F;1-37/Domain: signal sequence #status predicted <SIG>F;1-37/Product: insulin-like growth factor I alpha chain #status predicted <IGA>F;31-74/Product: insulin-like growth factor I bear chain #status predicted <IGB>F;91-974/Region: GPXY motif
F;971-974/Region: GPXY motif
F;988-1275/Domain: protein kinase homology <KIN>F;1006-1014/Region: protein kinase ATP-binding motif
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Search completed: June 29, 2004, 17:03:06 Job time : 15.2209 secs

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124 124 124 123 5 123 5 123 15 119 5 118 5 118 5	MOUSE PCCKS MOUSE STANDARD; PRT; 187 004592; Q62040; 01-FRB-1995 (Rel. 31, Created) 16-CCT-2001 (Rel. 40, Last sequence upd 15-MAR-2004 (Rel. 41, Last annotation up Proprotein convertase subtilisin/kexinn (Proprotein convertase PC5) (Subtilisin (Subtilisin-like proprotein convertase MAS musculus (Mouse).	Bukaryota; Metazoa; Chordata; Cran. Mammalia; Metazoa; Chordata; Cran. Mammalia; Butheria; Rodentia; Scius MCBI TaxID=10090; MCBI TaxID=10090; SEQUENCE OF 330-1877 FROM N.A. (ISC STRAIN=ICR; TISSUB=Intectine; MEDLINE=93327934; Pubmed=8335106; Makagama T., Murakami K., Nakayama "Identification of an isoform with Check a Kex2-like processing end FRES Lett. 327:165-171(1993).	SEQUENCE FROM N.A. (ISOFORM PC TISSUE-Brain, and Intestine; MEDLINE-9324489; PubMed-84683 Nakayawa T., Hosaka M., Torii. Nakayama R.; "Identification and functional mammalian Kex2-like processing Structural similarity to PACE4 J. Biochem. 113:132-135(1993).	UENCE FI SUB-Adre LINE-933 Bon J., NA STIM Addate I endocril C. Natl TIAL SE LINE-977 Bie I.,
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R InterPro; IPR0012884; Peptidase S8.

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InterPro; IPR0012884; Peptidase S8B.

R FinterPro; IPR001281; Processe Inhib.

R Pfam; PF01483; Peptidase S8; 1.

R PRINTS; PR00173; SUBTILISIN.

R PROSITE; PS00137; SUBTILIASE ASP; 1.

R PROSITE; PS00137; SUBTILIASE ASP; 1.

R PROSITE; PS00137; SUBTILIASE HIS; 1.

R PROSITE; PS00138; SUBTILIASE SER; 1.

R PROSITE; PS00139; SUBTILIASE SER; 1.
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Name=PCSB; Synonyma=Long;
IsoId=Q04592-1; Sequence=Displayed;
Name=PCSA; Synonyma=Long;
IsoId=Q04592-2; Sequence=USP_005439, VSP_005439;
IsoId=Q04592-2; Sequence=VSP_005439, VSP_005439;
IsoId=Q04592-2; Sequence=VSP_005439, VSP_005439;
-!- TISSUB SPECIFICITY: PCSA is expressed in most tissues but is most abundant in the intestine and adrenals. PCSB is expressed in the intestine, adrenals and lung but not in the brain.
-!- DEVELOPMENTAL STAGS: Weakly expressed throughout the embryo, except in the developing nervous system, the ribs and the liver, but markedly upregulated at discrete sites during development. At B6.5, prominent expression observed in differenciated decidua. At B7.5, intense expression in extraembryonic endoderm, amnion and nascent mesoderm. At B8.5, abundant expression in somites and yolk sac followed by a confination to dermamyotome compartment. Between B9.5 and B11.5, abundant expression in ARR (thickened ectodermal cells of limb buds). At B12.5, expression in the limbs is confined to the condeminal manual procession in the limbs is confined to the condeminal manual procession in the limbs is confined to the condeminal manual procession in the limbs is confined to the condeminal manual procession in the limbs is confined to the condeminal manual man
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                  DEVELOPMENTAL EXPRESSION.

MEDLINEs97436919; PubMed=9291583;

MEDLINEs97436919; PubMed=9291583;

Mancourt S.L., Rancourt D.B.;

"Murine subtilisin-like proteinase SPC6 is expressed during embryonic implantation, somitogenesis, and skeletal formation.";

Dev. Genet. 21:75-81(1997).

-! - FUNCTION: Likely to represent a widespread endoprotease activity within the constitutive and regulated secretory pathway. Capable of cleavage at the RX(K/R)R consensus motif. May be responsible for the maturation of gastrointestinal peptides. May be involved in the cellular proliferation of adrenal cortex via the activation of growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stage, strong expression also detected in vertebral and facial cartilage primordia and in the muscle of the tongue. At E16.5, abundant expression in epithelial cells of the intestinal villi. Isoform A is most abundant at all stages but significant levels of isoform B occur at E12.5.

DOMAIN: The propertide domain acts as an intramolecular chaperone assisting the folding of the zymogen within the endoplasmic
                                                                                                                                                                                                                                                                                                                              of growth factors.

CATALYTIC ACTIVITY: Release of mature proteins from their proproteins by cleavage of Arg-Yaa-ARG-|-Zaa bonds, where Xaa can be any amino acid and Yaa is Arg or Lys.

SUGCELLUTAR LOCATION: PCSA IS SECRETED THROUGH THE REGULATED SECRETORY PATHWAY. PCSB IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: AC 1 and AC 2 (clusters of acidic amino acids) contain sorting information. AC 1 directs TGN localization and interacts with the TGN sorting protein PACS-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Belongs to peptidase family S8. SIMILARITY: Contains 1 homo B/P domain.
     Cell Biol. 134:181-191(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLY ENDOSOMES.
ALTERNATIVE PRODUCTS:
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PROPROTEIN CONVERTASE SUBTILISIN/KEXIN

34 116 1877

fransmembrane

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1209 NOPCHSSCKTC---NGSLCASCPTGMYLWLQ-----ACVPSCPQG----TWPSVTSG 1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 KCTKCKVDCDTCFNKNPCTKCKS----GFYLHLGKCLDSCPEGLEANNHTMECVSIVHCB 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 ASEMSPWSPCMKKGKTCGPKRGTETRVRDIL-----QHPSAKGKGNLCPPTSETRTCIV 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 SQGCQGGCATCSDYNG -- CLSCKPRLPFVLBRIGMKQIGVCLSSCPSGYYGTRYPDI -- N 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                            42; Gaps
                                                                                                                                                                                                                                                                                                                    GBYIDDQGHCQTCEASCAKCWGPTQEDCISCPVTRVLD
ATBESWABGGFCMLVKKNNLCQRKVLQQLCCKTCTFQG
                                                                                                                                                                     (POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                      (BY SIMILARITY
                                                                                                                                    SIMILARITY
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                                                                      AC 1.
AC 2.
AC 2.
AC 2.
AC 2.
AC 4.
CLIADAGE (AUTO-) (BY SIMILARITY).
CELL ATTACHMENT SITE (POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY
CHARGE RELAY SYSTEM (BY SIMILARITY
CHARGE RELAY SYSTEM (BY SIMILARITY
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                                                           CYS-RICH MOTIF (CRM) REGION
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1877 AA; 209287 MW; EC850E2DF20BAIC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                     (In isoform PC5A).
P_005439.
 EXTRACELLULAR (POTENTIAL)
                      CYTOPLASMIC (POTENTIAL).
CATALYTIC.
                                                                                                                                                                                  (GLCNAC.
(GLCNAC.
(GLCNAC.
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Pred. No. 1.2e-05;
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              POTENTIAL.
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N-LINKED
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1 Similarity 27.8%;
52; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                      1877
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1877
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333
667
667
804
854
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Best Local S
Matches 52
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InterPro; IPR006212; Furin repeat. InterPro; IPR009030; Grow_fac_recep.

EMBL; D17583; BAA04507.1; -. D12619; BAA02143.1; -. EMBL; L14932; AAA74636.1; -

EMBL;

PIR; A48225; A48225. PIR; S34583; S34583. HSSP; Q99405; 1MPT. MEROPS; S08.076; MGD; MGI:97515; m

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                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20175281; PubMed=1070868;
A Oliva A.A. Jr., Chan S.J., Steiner D.F.;
I "Bvolution of the protocohordate amphioxus.";
I "Bvolution of the protocohordate amphioxus.";
I biochim. Biophys. Acta 1477:338-348(2000)
C -! FUNCTION: Likely to represent a widespread endoprotease activity
Within the constitutive and requiated secretory pathway. Capable
C -! CATALYTIC ACTIVITY: Release of mature proteins from their
proproteins by cleavage of Arg-Xaa-Yaa-ARG-|-Zaa bonds, where Xaa
C -: SUBCELLULAR LOCATION: ISOPORM A AND ISOPORM C ARE SECRETED.
ISOPORM B IS A TYPE I MEMBRANE PROTEIN.
                                                           Q9NJIS; Q9NJI4; Q9NJI6;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2003 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Proprotein convertase subtilisin/kexin type 5 precursor (BC 3.4.21.-)
(Proprotein convertase PC6-like) (aPC6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isold=Q9NJ15-3; Sequence=VSP 005442, VSP 005443; DOMAIN: The propeptide domain acts as an intramolecular chaperone assisting the folding of the zymogen within the endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;
Cleavage on pair of basic residues; Repeat; Alternative splicing;
                                                                                                                                                                                                                               Branchiostoma californiensis (California lancelet) (Amphioxus).
Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae.
Branchiostoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q9NJ15-2; Sequence=VSP_005444, VSP_005445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bvent=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to peptidase family S8-!- SIMILARITY: Contains 1 homo B/P domain.
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InterPro; IPR00930; Grow fac_recep.
InterPro; IPR00130; Grow fac_recep.
InterPro; IPR001309; Peptidase_S8.
InterPro; IPR001309; Peptidase_S8.
InterPro; IPR00130; Peptidase_S8.
InterPro; IPR00130; Peptidase_S8; I.Pfam; PP001483; P. Proprotein; I.Pfam; PP001483; Peptidase_S8; I.Pfam; PR00173; Peptidase_S8; I.Pfam; PR00173; Peptidase_S8; I.Pfam; S800131; SUBTILASE_ASP; FALSE_NEG.PROSITE; PS00139; SUBTILASE_HIS; I.Pfam; PROSITE; PS00139; SUBTILASE_SER; I.Pfam; I.Pfam; PROSITE; PS00139; SUBTILASE_SER; I.Pfam; I.Pfam; III.Pfam; III
                                            PRT; 1696 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q9NJ15-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS A; B AND C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
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                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25
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                                            PCK5 BRACL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1328 LHHGDCDSCHRECKTCDGPHHDNCLSCQPGSYLNDQQCSTHCPEGTFEFTYEDDSGETVL 1387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1504 Y--NČLSCPYGSKLGBGVCYPMČEBHKYYVEKTQICEEČDNSCKTČ---ŘĠ--STAHĎCĽ 1556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 DCDFCF--NKNFCTKCKSGFYLHLGKCLDSCPEGL--------EANN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 HTMBCVSIVH-----CEASEW----SPWSPCMKKGKTCGFKRGTETRVRDIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
                                                                                                                                                                                                                                                                                                                      DDTCTACNDGFL/IDASSCEAGCP -> ARKQNQASFCPFA
REWSVILABIALAGHHRYSLIDVPPQSNSPPDTVLGADRARL
TTATSAAGRCA (in isoform C).
/FTId=VSP_005442.
                                                                                                                                                                                                                                                                                                                                                                                         Missing (In isoform C).
/FIId=VSP 005443.
CHPTCKECSDEYDDTCTACNUCFLLIDASSCEAGCPPGQFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        HHGDCDSCHRBCKTC -> IARCVDRRDRSWCDLVLRFNFC
                                                                                                                                                                                                                                                                                                DDTILDRGECITSCGPGBYMDRREKKCKACHPTCKBCSDBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.8%; Score 181.5; DB 1; Length 1696; 23.9%; Pred. No. 2.6e-05; tive 23; Mismatches 72; Indels 121; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VRRYFVKRCCGTCKLYMEDRPMRRGSSQPTQGRN (in
               PROPROTEIN CONVERTASE SUBTILISIN/KEXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAC4 HUMAN STANDARD; PRT; 969 AA.
P29122; Q15099; Q15100; Q9URG7; Q9URJ1; Q9URJ2; Q9URJ7; Q9URJ9; Q9VR4G9; Q9Y4G9; Q9Y4H1; Q9URG29; Q9Y4G9; Q9Y4H1; Q1-DEC-1992 (Rel. 24, Created) 01-DEC-1992 (Rel. 24, Last sequence update) 15-MR-2004 (Rel. 44), Last annotation update) 15-MR-2004 (Rel. 44), Last annotation update) (SC 3.4.21.-) (Subtilisin/kexin-like protease PACE4) (Subtilisin/kexin-like protease PACE4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                  CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
                                                                                                                                                                                                                                         N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                   SIMILARITY)
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                                                                                                                                       CYS-RICH MOTIF (CRM) REGION.
CLEAVAGE (AUTO-) (BY SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1696 AA; 188410 MW; 281CBE1784257CBD CRC64;
                                                   EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Missing (in isoform A). /FIId=VSP 005445.
                                                                          POTENTIAL.
CYTOPLASMIC (POTENTIAL)
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                                                                                                            CATALYTIC.
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 POTENTIAL
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                                                       1618
1639
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1696
111
111
192
233
246
529
885
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Best Local Similarity
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                                                       DOMAIN
TRANSMEM
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CARBOHYD
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PAC4_HUMAN
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434:155-159(1998).

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Tsuji A., Hine C., Tamai Y., Yonemoto K., Mori K., Yoshida S., Bando M., Sakai E., Mori K., Akamatsu T., Matsuda Y.; "Genomic organization and alternative splicing of human PACE4 (SPC4), kexin-like processing endoprotease."; J. Biochem. 122:438-452(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Endoprocease PACE4 is Ca2+-dependent and temperature-sensitive and can partly rescue the phenotype of a furin-deficient cell strain."; Blochem. J. 339:639-647(1999).
                                                                                                   Identification of a second human subtilisin-like protease gene in the fes/fps region of chromosome 15.";
NA Cell Biol. 10:757-769(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nagahama M., Taniguchi T., Hashimoto B., Imamaki A., Mori K., Tsuji A., Matsuda Y.; "Biosynthetic processing and quaternary interactions of proprotein convertase SPC4 (PACB4).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS PACE4A-I; PACE4A-II; PACE4CS; PACE4D; PACE4E-I AND PACE4E-II).
MEDLINE-98021085; PubMed-9378725;
                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification of novel cDNAs encoding human kexin-like protease,
                                                                                                                                                                                                                                                       Matsuda Y.;
"Identification of novel cDNAs encoding human kexin-like protease
                                                                                                                                                                                                                                Feuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H., Atsuda Y.;
                                                                                                                                                                                                                                                                                                                                                                               Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUB=Placenta;
Mori K., Imamaki A., Kii S., Nagamune H., Nagahama M., Tsuji A.,
Mateuda Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Cerebellum;
MEDILINE-97335942; PubMed=9192737;
MEDILINE-97335942; PubMed=9192737;
Mori K., Kii S., Tsuji A., Nagamama M., Imamaki A., Hayashi K.,
Akamatsu T., Nagamune H., Matsuda Y.;
"A novel human PACE4 isoform, PACE4E is an active processing procontaining a hydrophobic cluster at the carboxy terminus.";
J. Biochem. 121:941-948(1997).
                                  TISSUE=Hepatoma, and Kidney;
MEDLINE=92075167; PubMed=1741956;
Kiefer M.C., Tucker J.B., Joh R., Landsberg K.E., Saltman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhong M., Benjannet S., Lazure C., Munzer S., Seidah N.G.; "Punctional analysis of human PACK4-A and PACK4-C isoforms identification of a new PACK4-CS isoform.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sucic J.F., Moehring J.M., Inocencio N.M., Luchini J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification of a novel PACB4 isoform, PACB4B.";
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS PACE4E-I AND PACE4E-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 204:1381-1382(1994)
                   FROM N.A. (ISOFORMS PACE4A-I AND PACE4B)
                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 200:943-950(1994)
                                                                                                                                                                                 FROM N.A. (ISOFORMS PACE4C AND PACE4D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE SPLICING (ISOFORM PACE4CS).
MEDLINE=97064242; PubMed=8906861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM PACE4A-II).
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                                                                                                                                                                                                TISSUE=Placenta;
MEDLINE=94235049; PubMed=8179631;
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95071480; PubMed=7980617;
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                                                                                                                                                                                                                                                                                             PACE4 isoforms.";
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isold=2012-8; Sequence=VSP_005436, VSP_005437;
TISSUS SPECIFICITY: Rach PACE4 isoform exhibits a unique restricted distribution. PACE4A-1 is expressed in heart, brain, placenta, lung, skeletal muscle, kidney, pancreas, but at comparatively higher levels in the liver. PACE4A-II is at least expressed in placenta. PACE4B was only found in the embryonic kidney cell line from which it was isolated. PACE4C and PACE4D are placenta. PACE4E-I is expressed in cerebellum, placenta and pitultary. PACE4E-II is at least present in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P29122-6; Sequence=VSP_005427, VSP_005434, VSP_005435; Note=Probably enzymatically Inactive;
                                                                                                                                                                                                                                                                 Name=PACB4A-11;
1801d=P29122-2; Sequence=VSP_005436;
Name=PACB4B; Synonyms=PACB4.1;
IsoId=P29122-3; Sequence=VSP_005428, VSP_005429;
                                                                                                                                                                                                                                                                                                                                      IsoId=P29122-4; Sequence=VSP 005432, VSP_005433;
Note=Probably enzymatically inactive;
                                                                                                                                                                                                                                                                                                                                                                           VSP_005431;
                                                                                                                                                                                                                           Bvent=Alternative splicing; Named isoforms=8;
Name=PACE4A-1; Synonyms=PACE4;
IsoId=P29122-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                              Note=Probably enzymatically inactive
                                                                                                                                                                                                                                                                                                                                                                          Isold=P29122-5; Sequence=VSP 005430, Note=Probably enzymatically Inactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=PACE4B-1;
IsoId=P29122-7; Sequence=VSP_005437;
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AB001904; 1
AB001905; 1
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respective precursors.
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                                                                                                                                                                                                                                                                                                                                                                             838 PDSELIRCGECHHTCGTCVGPGREECIHCAKNFHFHDWKCVPACGEGFFPEEMPGLPHKV 897
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P10432, Q24301;
P10-372, Q24301;
P10-072-2003 (Rel. 42, Last sequence update)
Purin-like procease 2 precursor (RC 3.4.21.75) (Furin 2).
FURZ OR CG18734/CG4235.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                11.7%; Score 179; DB 1; Length 969; 23.3%; Pred. No. 2.3e-05;
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TISSUE SPECIFICITY: Transient expression in a subset of central nervous system neurons during embryonic stages 12-13. Expression in developing tracheal tree from stage 13 to end of embryonic
                                                                                    DEVELOPMENTAL STAGE: Expressed both maternally and zygotically. SIMILARITY: Belongs to peptidase family S8. Furin subfamily.
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Multigene family; Zymogen; Repeat.
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CYTOPLASMIC (POTENTIAL).
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G0; G0:0004276; Fiturin activity; IDA.
InterPro; IRR005012; Furin repeat.
InterPro; IRR005013; Furin repeat.
InterPro; IRR00209; Peptidase_S8.
InterPro; IRR002084; Peptidase_S8.
InterPro; IRR002084; Peptidase_S8.
InterPro; IRR009020; Protease_Inhib.
Pfam; PF00483; P_proprotein; Z.
Pfam; PF00013; Peptidase_S8; 1.
PRINTS; PR00723; SUBTILISIN.
ProDom; PD000717; P_domain; 1.
SWART; SW00281; FU; 10.
PROSITE; PS00134; SUBTILASE_RS; 1.
PROSITE; PS00134; SUBTILASE_RS; 1.
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EMBL, L33831; AAA69860.1; --
EMBL, AE003502; AAF48598.1; --
PIR; A44434; A43434.
HSSP, Q99405; 1MPT.
MEROPS; S08.049; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINB=97166043; PubMed=9013936;
Zheng M., Seidah N.G., Pintar J.B.;
"The developmental expression in the rat CNS and peripheral tissues of
proceases PCS and PACE4 mRNAs: comparison with other proprotein
                                                                                                                                                                 1048 OFCPDGYFENSRNRTCVPCEPNCASCQDHPEYCTSCDHHLVMHEHKCYSACPLDTYETBD
                                                                 23 NASRGRRORRMHPN---VSQGCQGGCATCSDY--NGCLSCKPRLFFVLBRIGMKQIGVCL
                                                                                                                                -----GTRYPDI
                                                                                                                                                                                                  NKCTKCKVDCDTCF -- NKNFCTKCKSGPYLHLGKCLDSCPEGLBANNHTMBCVSIVHCBA
                                                                                                                                                                                                                                                                                                                                                                                               P41413; Q62914;
01-NOV-1995 (Rel. 32, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
(Proprotein convertase PC5) (Subtilisin/kexin-like protease PC5)
(rPC5) (PC6) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20214819; PubMed=10749928; Xiang Y., Molloy S.S., Thomas G.; Xiang Y., Molloy S.S., Thomas L., Thomas G.; Tect CGB cytoplasmic domain contains two acidic clusters that direct sorting to distinct trans-Golgi network/endosomal compartments."; Mol. Biol. Cell 11:1257-1273(2000).
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Adrenal gland;
MEDLINE=9314205; PubMed=8341687;
Lusson J., Vieau D., Hamelin J., Day R., Chretien M., Seidah N.G.;
"CDNA structure of the mouse and rat subtilisin/kexin-like PCS: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Adrenal gland;
De Bie I., Marcinkiewicz M., Nakayama K., Lazure C., Seidah N.G.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                72;
11.3%; Score 174; DB 1; Length 1679; 24.5%; Pred. No. 8.6e-05; ive 15; Mismatches 61; Indels 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM SHORT), AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      candidate proprotein convertase expressed in endocrine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nonendocrine cells.";
Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1676-1877 FROM N.A. (ISOFORM LONG).
                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1877 AA
                                                                                                                                                                                                                                                                                                   -----PCOEGCKTC 1169
                                                                                                                                                                                                                                                                    151 SEWSPWSPCMKKGKTC 166
Query Match 11.3
Best Local Similarity 24.5
Matches 48; Conservative
                                                                                                                                SSCPSGYY-----
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                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                78
                                                                                                                                                                                                  93
                                                                                                                                                                                                                                                                                                   1161
                                                                                                                                                                                                                                                                                                                                                                                    PCKS RAT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
proproteins by cleavage of Arg-Xaa-Yaa-ARG-|-Zaa bonds, where Xaa can be any amino acid and Yaa is Arg or Lys.
SUBCELLUIAR LOCATION: PCSA IS SECRETED THROUGH THE REGULATED SECRETORY PATHWAY. PCSE IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH BARLY ENDOSOMES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                      -!- DCWAIN: AC 1 and AC 2 (clusters of acidic amino acids) contain sorting information. AC 1 directs TGN localization and interacts with the TGN sorting protein PAGS-1.
-! SIMILARITY: Belongs to peptidase family S8.
-!- SIMILARITY: Contains 1 homo B/P domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR0062012; Furin repeat.

R InterPro; IPR002099; Peptidase S8.

R InterPro; IPR002099; Peptidase S8.

R InterPro; IPR001209; Protease Inhib.

R InterPro; IPR0012019; Protease Inhib.

Pfam; PR001433; P proprotein; I.

R PROMO723; SUBTILISIN.

R PROSTITE; PR00137; SUBTILIASE ASP; 1.

R PROSTITE; PR00139; SUBTILIASE ASP; 1.

R PROSTITE; PR00139; SUBTILIASE ASP; 1.

R PROSTITE; PR00139; SUBTILIASE BRR; 1.

R Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
PROPROTEIN CONVERTASE SUBTILISIN/KEXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYS-RICH MOTIF (CRM) REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
CYTOPLASMIC (POTENTIAL)
CATALYTIC.
HOWO B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; 114933; AAA99906.1; -. EMBL; U47014; AAA87888.1; -.
                                                                          ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34
116
1877
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1789
1877
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602
1753
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HSSP; Q99405; 1MPT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117
1769
1790
                                                                                                                                                                                                                                                                                                                                                                   reticulum
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TRANSMEM
DOMAIN
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                683 ADKKRCRKCAPNCESCFGSHADQCLSCKYGYPINEFISSCVAQCPEGSYQDIKKNIC--- 739
                                                                                                                                                                                                                                                                                                                                                                                                                                            83
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MEDLINE-20363723; PubMed=10903434;
Thacker C., Srayko M., Rose A.M.;
"Mutational analysis of bli-4/kpc-4 reveals critical residues required
                                                                                                                                                                                                                                                                                                                                                                                                                                            35 PNVSQ-GCQG----GCATCSDYNGCLSCKPRLPPVLERIGMKQIGVCLSSCPSGYYGTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           640 PECSEVGCDGPGPDHCTDCLHYHYKLKNNTR------ICVSSCPPGHF---H
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cuticle protein 4).
BLI-4 OR KPC-4 OR KO4F10.4.
Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                          ATERSWARGGFCMLVKKNINLCQRKVLQQLCCKTCTPQG
                                                        CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLI4_CAREL STANDARD; PRT; 943 AA.
P51559; O44762; O44764; O44765; O44766;
01-0CT-1996 (Rel. 34, Created)
10-0CT-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Endoprotease bli-4 precursor (BC 3.4.21.-) (Blisterase) (Blistered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 VHCRASEWSPWSPCMKKGKTC-GPKRGTETRVRDILQHPSAKGKGNLCPPTSE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------GKCSENCKTCTGPHNCTECKGGLSLQ------GSRCSVTCB 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thacker C., Peters K.W., Srayko M., Rose A.W., ethe bli-4 locus of Caenorhabditis elegans encodes structurally distinct kex2/subtilisin-like endoproteases essential for early
                                                                                                                                                                                                                                                                                                                                                                                                              48;
                       CELL ATTACHMENT SITE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                        10.7%; Score 164; DB 1; Length 1877; 27.7%; Pred. No. 0.00047; tive 20; Mismatches 57; Indels 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEGUENCE FROM N.A. (ISOFORMS A; B; C AND D), AND FUNCTION STRAIN-Bristol N2; MEDLINE-95293228; PubMed=7774813;
                                                                                                                                                                                                                                                                                                                                          1877 AA; 207888 MW; 890955DC60534444 CRC64;
                                                                                                                                                                                                                                                                                                         Missing (in isoform PC5A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Latreille P., Wamsley P.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                            (in isoform PCSA)
/PTId=VSP_005440.
                                                                                                                                                                                                                                                                                                                          PTIG=VSP_005441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        development and adult morphology."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genes Dev. 9:956-971(1995)
                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 27.7
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                             1877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                             916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6239;
                                                                                                                                           CARBOHYD
CARBOHYD
CARBOHYD
                                                              ACT SITE
ACT SITE
ACT SITE
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CARBOHYD
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DOMAIN
DOMAIN
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Matches
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                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EWBL outstation. the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sib.sib.ch).
                                                                                                                                                                                  WormDep; NG4F10.45; CB11728.

R WormDep; KG4F10.44; CB11728.

R WormDep; KG4F10.44; CB11730.

R WormDep; KG4F10.44; CB11732.

R WormDep; KG4F10.44; CB11732.

R GO; GO: 00101621; CS11736.

R GO; GO: 00101522; F: Serine-type endopeptidase activity; NAS.

GO; GO: 0007522; F: Serine-type endopeptidase activity; NAS.

R GO; GO: 0007522; F: Serine-type endopeptidase activity; NAS.

R GO; GO: 0007522; F: Serine-type endopeptidase activity; NAS.

R InterPro; IPR00212; Purin repeat.

R InterPro; IPR00209; Poptidase SBB.

R InterPro; IPR00209; Poptidase SBB.

R InterPro; IPR00910; Protease Inhib.

R Pfam; PP00181; P_proprotein; I.

R Pfam; PP00182; Peptidase SB; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00136; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00139; SUBTILASE BRR; 1.
Hydrolase; Serine protease; Glycoprotein; Calcium-binding; Zymogen;
Transmembrane; Signal; Alternative splicing.
for proprotein convertase function in C. elegans.";
Gene 252:15-25(2000).
-!- FUNCTION: The Kex2/subtilisin-like proteinase activity of this enzyme is required for the normal production of adult cuticle. There is functional redundancy between the isoforms. Vital for embryonic and larval development.
-!- ALTERNATUR PRODUCTS:
EVENT.-ALTERNATUR PRODUCTS:
EVENT.-ALTERNATUR PRODUCTS:
EVENT.-ALTERNATUR PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENDOPROTEASE BLI-4.
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                          Name=A; Synonyms=a;
IsoId=P51559-2; Sequence=VSP_005416, VSP_005419;
Name=B; Synonyms=b;
IsoId=P51559-3; Sequence=VSP_005418, VSP_005421;
Name=C; Synonyms=c;
IsoId=P51559-4; Sequence=VSP_005422, VSP_005423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
                                                                                                 IsoId=P51559-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00723; SUBTILISIN.
ProDom; PD000717; P domain; 1.
SMART; SM00261; FU; 3.
                                                                                     Name=D; Synonyms=d;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
ACT_SITE
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721 Y----YLDGDKCKACSSHCHTCTKAEVCETCPGSLLLIDVDNMPHYDHGKCVESCPPGLV 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      663 RSSFPDLTSGWKLSCDECNGGCTESSSATSCFAYK-HLTQTLRNKGGSGF-KCVQKCDDT 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 YYGTRYPDINKCTKCKVDCDTCPNKNPCTKCKSGFYL-----HL--GKCLDSCPEGLE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                777 ADYES----NLVQAK------CIWRKDLCGDG------YYINAVGKCDLCDS 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 ANNHIWECVSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDILQHPSAKGKGNLCPP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 RRMHPNVSQG------CQGGCATCSDYNGCLSCKPRLFFVLERIGMKQIGVCLSSCPSG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             828 // COSTAL OSTAL OSTA
                                                                                                                                                                                                                                                isoform A).
/FTId=VSP 005416.
FTID=VSP 005416.
L -> LCFNPENSQPTECVCLRVCEPGVIINFQIEKLKKST
KCLIFS (in isoform E).
/FTId=VSP 005417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEESARSSFPDLTSGWKLSCDECNGGCTESSSATSCFAYKH
TYTLANGSGSGFKCVGCDOTYTDGDKCKT -> GDEVV
ERIRNHWEVTLEESSHWNWELARBHKSLOFLANSSSTTHSPL
YSFTKFQPIPLILVCIPDAIHRQFAV (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76; Indels 48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Paired basic amino acid cleaving enzyme 4 precursor (BC 3.4.21.-)
(Subtilisin/kexin-like protease PACE4) (Subtilisin-like proprotein
PACE4.
(BY SIMILARITY)
(BY SIMILARITY)
                                                                                                                                                                                                               VBESARSSPPDLT -> ILITIAIHLVVNA (in
                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 10.6%; Score 162; DB 1; Length 943; Best Local Similarity 27.1%; Pred. No. 0.00034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Missing (In isoform A).
/FTId=VSP 005419.
Missing (In isoform E).
/FTId=VSP 005420.
                                                                                                     CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Missing (In isoform B). /FIId=VSP_005421.
       CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VSP 005418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         937 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 TSETRIC--IVQRKKCSKG 211
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943 AA;
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            WEDLINE=9449873; PubMed=8000361;
Johnson R.C., Darlington D.N., Hand T.A., Bloomquist B.T., Mains R.E.;
Johnson R.C., Darlington D.N., Hand T.A., Bloomquist B.T., Mains R.E.;
Johnson R.C., Darlington D.N., Hand T.A., Bloomquist B.T., Mains R.E.;
pituitary and regulated by thyroid status.";

Endocrinology 135:1178-1185(1994).

-! FUNCTION: Likely to represent an endoprotease activity within the constitutive secretory pathway, with unique restricted distribution in both neuroendocrine and non-neuroendocrine tissues and capable of cleavage at the RK[K/R]R consensus motif.

-! CATALTITE CATALTITE:

proproteins by cleavage of Arg-Kaa-Yaa-ARG-|-Zaa bonds, where Xaa can be any amino acid and Yaa is Arg or Lys.
                                                                                                                                                                                                                                                     COPACTOR: Calcium (Potential).
TISSUB SPECIFICITY: High expression in the anterior pituitary and in several brain regions, the atrium, and the ventricle DOMAIN: The propeptide domain acts as an intramolecular chaperone assisting the folding of the zymogen within the endoplasmic
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CLEAVAGE (AUTO-).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
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PROSITE; PSSO900; PLAC; 1.
PROSITE; PSSO901; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal; Calcium; Cleavage on pair of basic residues; Repeat.
POTENTIAL.
STRAIN-Sprague-Dawley; TISSUE-Hypothalamus, and Pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYS-RICH MOTIF (CRM) REGION
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                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to peptidase family $8. -!- SIMILARITY: Contains 1 homo B/P domain. -!- SIMILARITY: Contains 1 PLAC domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR006212; Furin repeat.
InterPro; IPR001209; Peptidase S8.
InterPro; IPR0012894; Peptidase S8.
InterPro; IPR0091201; Peptidase S8.
InterPro; IPR00912; Peptidase S8.
Pfam; PF01483; Proprotein; I.
PRINTS; PR00723; SUBTILISIN.
PRODOM; PD000717; P domain; 1.
SWART; SW00261; FU; 5.
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MEROPS; S08.075; -.
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CLSSCPSGYYGTRYPDINKCTKCKVDCDTCPNK-NPCTKCKSGFYLHLGKCLDSCPEGLE 134
                                                                                                                                                     135 ANNHIMEC-----PWSP 158
                                                                                                                                                                                           806 PDSELIRCGECHHTCRICVGPSREBCIHCAKSPHFQDWKCVPACGEGFYPBEMPGLPHKV 865
                                                                                                                                                                                                                                        159 CHKKGKTC----GFKRG-----TETRVRDILQHPSAKGKGNLCPPTSBTRTCIVQRK 206
                                                                                                                                                                                                                                                                               866 CRRCDENCLSCEGSSENCSECKAGFIQLGTSCITNHTCSNADETFCEMVKSNRLC--ERK 923
                                                                                            Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-) (Proprotein convertase PC5) (Subtilisin/kexin-like protease PC5) (PC6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- PUNCTION: Likely to represent a widespread endoprocease activity within the constitutive and regulated secretory pathway. Capable of Cleavage at the RX(K/R) consensus motif.
-i- CATALYTIC ACTIVITY: Release of mature proteins from their proproteins by cleavage of Arg-Xaa-Yaa-ARG-|-Zaa bonds, where Xaa can be any amino acid and Yaa is Arg or Lys.
-i- SUBCELLULAR LOCATION: Secreted (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=092824-1; Sequence=Displayed; 1758UB SPRCIFICITY: Expressed in T-lymphocytes. DOMAIN: The propeptide domain acts as an intramolecular chaperone assisting the folding of the zymogen within the endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=6635380; PubMed=8755538; Miranda L., Wolf J., Pichuantes S., Duke R., Franzusoff A.; Miranda L., Wolf J., Pichuantes S., Duke R., Franzusoff A.; Insolation of the human PCG gene encoding the putative host protease for HIV-1 gpl60 processing in CD4+ T lymphocytes."; Proc. Natl. Acad. Sci. U.S.A. 93:7695-7700(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Franzusoff A., Miranda L., Wolf J., Pichuantes S., Lu Y., Duke Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reudelhuber T.L.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
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Comment=2 isoforms may be produced;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to peptidase family S8. SIMILARITY: Contains 1 homo B/P domain. SIMILARITY: Contains 1 PLAC domain.
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-MRR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                             913 AA
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10.5%; Score 161; DB 1; Length 937; 22.5%; Pred. No. 0.0004;

12; 75

72; Gaps

90; Indels

24; Mismatches

Conservative

Local Similarity 54;

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                                                       PIRE, GOZ428; GOZ428.

BRENDES, 299405; IMPT.

RENGES, SO8.076; --

RENGES, CEXTRACELLULAR SPACE, TAS.

RO; GO:000526; P: P: Cell-cell signaling; TAS.

RO; GO:0007267; P: Cell-cell signaling; TAS.

RO; GO:0007267; P: Cell-cell signaling; TAS.

RO; GO:0007267; P: Proteine-type endopeptidase activity; TAS.

RO; GO:0007267; P: Proteine-type endopeptidase activity; TAS.

RICEPPO: IPR00209; Proteine-TS.

RICEPPO: IPR00209; Proteine-S8.

INTERPO: IPR00309; Proteine-S8.

INTERPO: IPR00309; Proteine-S8.

REAM: PR0013; PR01483; P. Proteine-S8; 1.

REAM: PR0017; P. domain; 1.

REAM: PR0017; P. domain; 1.

REAM: PR0017; P. SOBTILASE_HIS; 1.

RROSITE; PS00137; SUBTILASE_HIS; 1.

RROSITE; PS00137; SUBTILASE_HIS; 1.

RROSITE; PS00137; SUBTILASE_HIS; 1.

RROSITE; PS00137; SUBTILASE_HIS; 1.

RROSITE; PS00138; SUBTILASE_HIS; 1.

RROSITE; PS00137; SUBTILASE_HIS; 1.

RROSITE; PS00138; SUBTILASE_HIS; 1.

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CYS-RICH MOTIF (CRM) REGION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC.
or send an email to license@isb-sib.ch)
                             EMBL; U56387; AAC50643.2; -. EMBL; U49114; AAA91807.1; -.
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                                                                                                                                                                                                                                                                                                                                       141 ECVSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDILQHPSAKG-KGNLC----P 193
                                                                                                                                                                                                                                                                                                                                                                        307
                                                                                                                                                                                                                                                                                                                                                                                                         194 PISETRICIVQRK-KCSKGERGKKGRERKRKLANKEERKETSSSSDSKGLESSIETPDQQ 252
                                                                                                                                                                                                                                      CTGGCRNGGFCNDRHVCECPDGFYGPHCEKALCMPRCM-----NGGLCVTPGLCIC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                         308 SCGAHGTCIBPNKCQCKEGWNG-----RYCNKKYGSNLMNALRPTGSRNRQHTPSPK 359
                                                                                                                                                                                                     41 CQGGCAT---CSDYNGC----LSCKPRLFFVLRRIGMKQIGVC---LSSC 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. 187:934-939(1992).
-!- FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF I)
WITH A HIGH APPINITY AND IGF II WITH A LOWER APPINITY. IT HAS A
                                                                                                                                                                                                                                                                                                                                                          78; Indela 85; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIANE=95277910; PubMed=7758167;
Du J., Delafontaine P.;
"Inhibition of vascular smooth muscle cell growth through antisense
transcription of a rat insulin-like growth factor I receptor CDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leroith D.; \label{eq:control} \mbox{"Developmental regulation of the rat insulin-like growth factor I}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Werner H., Woloschak M., Adamo M., Shen-Orr Z., Roberts C.T. Jr.,
                                               POTENTIAL.
N-LINKED (GLCNAC. . ) (POTENTIAL)
N-LINKED (GLCNAC. . ) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-1992 (Rel. 21, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FSB-2003 (Rel. 41, Last amnotation update)
Insulin-like growth factor I receptor precursor (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 913-1017 FROM N.A.
MEDIJINE-22412145; PubMed=1530648;

Kurachi H., Jobo K., Johta M., Kawasaki T., Itoh N.;

Kurachi H., Jobo K., Johta M., Kawasaki T., Itoh N.;

Kanachi H., Jobo K., Johan M., Kawasaki T., Itoh N.;

Kurachi H., Jobo K., Johan M., Kawasaki T., Itoh N.;

Feceptor.related receptor, is expressed preferentially in the
                                                                                                                                 10.0%; Score 153.5; DB 1; Length 374; 24.4%; Pred. No. 0.00056;
                                                                                                 41071 MW; B26F973B0F00ACFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor gene.";
Proc. Natl. Acad. Sci. U.S.A. 86:7451-7455(1989)
                                                                                                                                                                    23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1370 AA.
                 POTENTIAL. POTENTIAL.
 POTENTIAL
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MEDLINE-90017496; PubMed-2477843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Circ. Res. 76:963-972(1995).
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                                                                                                                                                                    60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
 291
309
315
323
83
240
                                                                                240
374 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 ENKERQ 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 RTEDRÓ 365
                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
               DISULPID
                                                DISULPID
                                                                                  CARBOHYD
                                                                                                                                                                                                                                     177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IG1R_RAT
P24062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kidney.";
                                                                                                                                    Query Match
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                tyrosine phosphate.
SUBGINIT: TETRAMEN OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-BINDING DOMAIN, WHILE THE BETA CHAIN CARRIES THE KINASE DOMAIN.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                              INSULIN-LIKE GROWTH PACTOR I RECEPTOR,
                                                                                                                                                                                                      INSULIN-LIKE GROWTH FACTOR I RECEPTOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
TYROSINE-PROTEIN KINASE ACTIVITY.
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                  SIMILARITY: Contains 2 fibronectin type III domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
PROTEIN KINASE.
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N-LINKED (GLCNAC...
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ATP (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BETA-CHAIN.
                                                                                                                                                                                EMBL; L29232; AAA41392.1; -.
EMBL; M27293; AAA41384.1; -.
HSSP; P06213; IIRK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1370
                                                                         receptor subfamily
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DISULPID
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BINDING
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DISULPID
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                                                                                                                                                                                                                                                                                                                                                                                                                    94 KCTKCKVDCDTCFN-KNFCTKCKSGFYLHLGKCLDSCPEGLEANN-HTMECVSIVHCEAS 151
                                                                                                                                                                                                                                                                                                                                   34 HPNVSQGCQGGCATCSDYNGCLSCKPRLFFVLERIGMKQIGVCLSSCPSGYYGTRYPDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Embryo;
MEDLINE-9376785; PubMed-8367492;
MEDLINE-93776785; PubMed-8367492;
Ruiz i Altaba A., Cox C., Jessell T.M., Klar A.;
Ruiz i Altaba A., Cox C., Jessell T.M., Klar A.;
"Ectopic neural expression of allow plate marker in frog embryos injected with the midline transcription factor Pintallavis.";
Proc. Natl. Acad. Sci. U.S.A. 90:8268-8272(1993).
-!-FUNCTION: Promoces the attachment of spinal cord and sensory neuron cells and the outgrowth of neurites in vitro. May contribute to the growth and guidance of axons in both the spinal cord and the PNS.
                                                                                                                                                                                                                                                                                                    57; Indels 40; Gaps
                                                                                                                                                                                                       66 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
86 AD -> PY (IN RBF. 3).
155395 MM; A5946897A41CB145 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed at high levels in the floor plate.
-!- SIMILARITY: Contains 6 TSP type-1 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                            (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
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(POTENTIAL)
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(POTENTIAL)
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                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                   9.7%; Score 149; DB 1; Length 1370; 28.7%; Pred. No. 0.0039; tive 20; Mismatches 57; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 EWSPWSPCMKKGKTCGFKRGTETRVRDILQHPSAKG----KGNL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----GPC---PKVCGDEBKKTKTIDSVTSAGMLQGCTILKGNL 361
                                                                                                                                                                          (GLCNAC.
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01-JUN-1994 (Rel. 29, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
              N-LINKED
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                                                                                                                                                                                                                                                                                                    47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                     1370 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-spondin precursor
                                                                                                                                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                   232
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                                                           CARBOHYD
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SEQUENCE
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 CKPRLFFVLB------RIGMKQIGVCLSSCPSGYYGTR-YPDINKCTKCKV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 606 TIPCVLSPWSEWSDCSVTCGKGTRTRQR----MLKSPSBLGDCNBELBLKQVEKCMLPBCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----DCDTCFNKNFCTXCKSGFYLHLGKCLDSCPEGLEANN----HTMECV
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
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-!- FUNCTION: Functions as a receptor for membrane-bound ligands
Jaggedl, Jagged2 and Deltal to requlate cell-fate determination.
Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21331789; PubMed=11438922;
Irvin D.K., Zurcher S.D., Maynen T., Weinmaster G., Kornblum H.I.;
Expression patterns of Notchl, Notch2, and Notch3 suggest multiple
functional roles for the Notch-DSL signaling system during brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53;
                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
D3A54B329548AED9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.5%; Score 145.5; DB 1; Length 803; 26.6%; Pred. No. 0.0041; ive 23; Mismatches 84; Indels 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NTC2 RAT

ID NTC2 RAT

STANDARD; FRT; 2471 AA.

10 NTC2 RAT

STANDARD; FRT; 2471 AA.

11 O STANDARD; FRT; 2471 AA.

12 O STANDARD; FRT; 2471 AA.

13 O STANDARD; FRT; 2471 AA.

14 O STANDARD; FRT; 2471 AA.

15 O STANDARD; FRT; 2471 AA.

16 O STANDARD; FRT; 2471 AA.

17 O STANDARD; FRT; 2471 AA.

18 O STAND
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                                                                                                                                                              Cell adhesion.
                                                                                                                                                                                 POTENTIAL.
F-SPONDIN.
TSP TYPE-1 1.
TSP TYPE-1 2.
TSP TYPE-1 3.
TSP TYPE-1 4.
TSP TYPE-1 4.
TSP TYPE-1 6.
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MEDLINE=93202015; PubMed=1295745;
Medimaster G., Roberts V.J., Lemke G.;
"Notch2: a second mammalian Notch gene.";
Development 116:931-941(1992).
                              Pfam; PF02014; Reeler; 1.
Pfam; PF00090; tsp_1; 6.
SMART; SM00209; TSP1; 6.
PR0STE; PS50092; TSP1; 6.
Glycoprotein; signal; Repeat
InterPro; IPR002861; Reeler.
InterPro; IPR000884; TSP1.
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                                                                                                                                                                                                                                                                                        552
608
664
750
210
677
803 AA;
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Les 58; Conserv
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NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 2.
NOTCH EXTRACELLULAR TRUNCATION (BY
SIMILARITY).
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CALCIUM-BINDING (POTENTIAL)
CALCIUM-BINDING (POTENTIAL)
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                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                  | SGF-LIKE 1. | SGF-LIKE 1. | SGF-LIKE 2. | SGF-LIKE 3. | SGF-LIKE 4. | SGF-LIKE 4. | SGF-LIKE 4. | SGF-LIKE 5. | CALCIUM-BINDING (PO EGF-LIKE 9. | CALCIUM-BINDING (PO EGF-LIKE 9. | CALCIUM-BINDING (PO EGF-LIKE 10. | CALCIUM-BINDING (PO EGF-LIKE 11. | CALCIUM-BINDING (PO EGF-LIKE 11. | CALCIUM-BINDING (PO EGF-LIKE 12. | CALCIUM-BINDING (PO EGF-LIKE 13. | CALCIUM-BINDING (PO EGF-LIKE 13. | CALCIUM-BINDING (PO EGF-LIKE 13. | CALCIUM-BINDING (PO EGF-LIKE 23. | CALCIUM-BINDING (PO EGF-LIKE 33. | CALCIUM-B
                                                                            NOTCH INTRACELLULAR DOMAIN (BY
                                                                                                               EXTRACELLULAR (POTENTIAL)
                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
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LIN/NOTCH 1.
LIN/NOTCH 1.
LIN/NOTCH 2.
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ANK 2.
ANK 3.
ANK 4.
ANK 6.
BY SIMILARITY.
                                                                                                   SIMILARITY)
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POLY-LEU.
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       **C. -1- DEVELOPMENTAL STAGES: Expressed in the brain during E14 and E17.

-1- DEVELOPMENTAL STAGES: Expressed in the brain during E14 and E17.

-1- PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertage in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(FK). Following Ilgand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presentilin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane (By similarity).

--- FTM: Phosphorylated (By similarity).

--- SIMILARITY: Contains 35 EGP-like domains.

--- SIMILARITY: Contains 2 Lin/Notch repeats.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H HSSP; P00743; 1CCP.

R HSSP; P00743; 1CCP.

R InterPro; IPR0001210; AMK.

R InterPro; IPR0001210; AMK.

R InterPro; IPR0001881; EGF_Ca.

R InterPro; IPR001881; EGF_Ca.

R InterPro; IPR001881; EGF_Ti.

R InterPro; IPR001809; EGF_Ti.

R InterPro; IPR002049; LamInin_EGP.

R InterPro; IPR002049; LamInin_EGP.

R InterPro; IPR002049; LamInin_EGP.

R Pfam; PP00068; EGF_Ti.

R Pfam; PP00068; EGF_Ti.

R Pfam; PP00066; notch; 2.

Pfam; PP00066; notch; 3.

Pfam; PR00019; EGFBLOOD.

R PRINTS; PR00011; EGFLAMININ.

R PRNNTS; PR00119; EGF_CA; 24.

SWART; SW00044; ANK REP REGION; 1.

PROSITE; PS00029; ANK REPERT; 2.

R PROSITE; PS00029; ANK REPERT; 2.

R PROSITE; PS00029; ANK REPERT; 3.

R PROSITE; PS01186; EGF_1; 34.

R PROSITE; PS01187; EGF_CA; 22.

R PROSITE; PS01187; EGF_CA; 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M93661; AAK13558.1; -. PIR; A49128; A49128.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 SAKGKGNI,CPPTSETRTCIVQRKKCSKGE-----RGKKGRERKRKKKLINKEE---- 229
                                                                                                                                                                                                                                                                                                                                                                                                                                            126 LDSCPEGLEANNHTM--ECVSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDILQHP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 -----RKETSSSDSKGLESSIETPDQQENKERQQQQKRRARD-----KQQKSVSVS 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              700 QFGGAP--CPET------VQRKKCRARKCLRSPSIQKLAWREARESRRSEQLREBSDGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            647 LGDCNEDLEQAEKCMLPECP--IDCELSEWSQWSEC---NKSCG--KGHMIRTRIIQMEP
                                                                                                                                                                                                                                                                                                                                                                                                                   53; Gaps
                                                                                                                                                                                                                                 POTENTIAL.
P.SPONDIN.
TSP TYPE-1 1.
TSP TYPE-1 2.
TSP TYPE-1 3.
TSP TYPE-1 4.
TSP TYPE-1 4.
TSP TYPE-1 6.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGIR MOUSE STANDARD; PRT; 1373 AA.

Q60751; 070438; Q62123;
01-NOY-1997 (Rel. 35, Created)
11-007-2001 (Rel. 40, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Insulin-like growth factor I receptor precursor (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                        Query Match 9.1%; Score 142.5; DB 1; Length 807; Best Local Similarity 29.5%; Pred. No. 0.0066; Matches 54; Conservative 16; Mismatches 60; Indels 53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Navarro M., Garandel V., Barenton B., Bernardi H.;
"Cloning of cDNA for the mouse insulin-like growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                         LINKED (GLCNAC. . .) (P. 309525F9EAFEA89A CRC64;
                                                                                                                                                                                                                      Cell adhesion.
                                                                                                             EMBL; M88469; AAA41174.1; --
PIR; A38152; A38152.
InterPro; IPR002861; Reeler.
InterPro; IPR000884; TSP1.
Pfam; PP02014; Reeler; 1.
Pfam; PF00090; tsp_1; 6.
SMART; SM00209; TSP1; 6.
Glycoprotein; Signal; Repeat; 6.
SIGNAL
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SEQUENCE OF 1-329 FROM N.A.
STRAIN=CD-1; TISSUE=Kidney;
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                                                                                                                                                                                                                                                                                                                                                     681 6
807 AA;
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                                                                                                                                                                                                                                                                                                                                                                                   947 QTDMARCLSBPCKNG-GTCSDYVNSYTC-------TCPAGFRGVHC 984
                                                                                                                                                                                                                                                                                                                                                                                                                   90 P-DINKCTKCKVDCDTCFNKNFC------TKCKSGFYLHLGK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 CLD-----SCPEGLEANNHTMECVSIVH-CEASEWSPWSPCMKKGKTCGFKRGTETRV 176
                                                                                                                                                                                                                                                                                                                                                                 30 ORRMHPNVSQGCQGGCATCSDYNGCLSCKPRLPPVLERIGMKQIGVCLSSCPSGYYGTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurite extension.";
Cell 69:95-110(1992).
-!- FUNCTION. Promotes the attachment of spinal cord and sensory
neuron cells and the outgrowth of neurites in vitro. May
contribute to the growth and guidance of axons in both the spinal
                                                                                                                                                                                                                                                                                                                                         87; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F-spondin precursor.
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cord and the PNS.
SUBCELLULAR LOCATION: Secreted.
TISSUB SPECIFICITY: Expressed at high levels in the floor plate.
SIMILARITY: Contains 6 TSP type-1 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUB-Embryonic floor plate;
MEDLINE-92208952; PubMed-1555244;
Klar A., Baldassare M., Jessell T.M.;
"F-spondin: a gene expressed at high levels in the floor plate encodes a secreted protein that promotes neural cell adhesion and
                                                                                                                                                                                                                                                                                                              ; Score 144.5; DB 1; Length 2471;
; Pred. No. 0.014;
25; Mismatches 54; Indels 87;
                                                                                                                                                                                                                                                                                                                         , 014;
.aa 54; Indels
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28-PBB-2003 (Rel. 41, Last annotation update)
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  01-JUN-1994 (Rel. 29, Created)
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 Local Similarity
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MEDIANE-90152381; PubMed-2482828;

WILLS A.F., Kurban R.R., Hovens C.M., Ralph S.J.;

WILLS A.F., Kurban R.R., Hovens Chain reaction to cloning members of the protein tyrosine kinase family.";

of the protein tyrosine kinase family.";

C.I. PUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF I)

TYROSINE-FROTENIN KINASE ACTIVITY.

C.I. CHALYTIC ACTIVITY: AND IGF II WITH A LOWER AFFINITY. IT HAS A TROSINE PROPERING FOR THE PROPERING CONTINUINTY.

C.I. CHALYTIC ACTIVITY: AND 1 SETA CHAINS LINKED BY DISULFIDE BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORWATION OF THE LIGAND-BINDING DOWAIN, WHILE THE BETA CHAIN CARRIES THE KINASE DOWAIN.

C.I. SUBCELLULAR LOCATION: Type I membrane protein.

C.I. SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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INSULIN-LIKE GROWTH FACTOR I RECEPTOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INSULIN-LIKE GROWTH PACTOR I RECEPTOR
Jun W., Liu Z., Alvares K., Kumar A., Wallner B.I., Kanwar Y.S.; Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probom; PD000001; Proc Kinase; 1.
SWART; SM00060; FN3; 3.
SWART; SM00060; FN3; 3.
SWART; SM000219; TU; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS002011; PROTEIN KINASE DOM; 1.
PROSITE; PS00239; RECEPPOR TYR KIN II; 1.
Transferase; Tyrosine-protein Kinase; Receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; ATP-binding; Phosphorylation; Repeat; Signal.
SIGNAL 31 741 INSHIAN-LIKE CENTER ENTER INSTITUTE.
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POTENTIAL.
CYTOPLASMIC (BY SIMILARITY).
FIBRONECTIN TYPE-III 1.
PIBRONECTIN TYPE-III 2.
PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BETA-CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:9643; IGFIT.
GO; GO:009807; P:organogenesis; IMP.
InterPro; IPR000494; EGFR_L_domain.
InterPro; IPR0003957; FN III-like.
InterPro; IPR001951; FN III-like.
InterPro; IPR005211; Puzin-like.
InterPro; IPR005212; Puzin repeat.
InterPro; IPR00512; Puzin repeat.
InterPro; IPR000719; Prot kinase.
InterPro; IPR00179; Prot kinase.
InterPro; IPR00179; Prot kinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR008266; Tyr_pkinase.AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfan; PF00041; fn3; 2.
Pfan; PF00041; fn3; 2.
Pfan; PF00057; Purin-like; 1.
Pfan; PF01030; Recep L domain; 2.
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; APOSG187; AAC12782.1; --
EMBL; U00182; AAC52123.1; --
EMBL; M3422; AAA40013.1; --
PIR; A48805; A48805
HSSP; PO6213; IIRK
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94 KCTKCKVDCDTCFN-KNFCTKCKSGFYLHLGKCLDSCPEGLEANN-HTMECVSIVHCEAS 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 HPNVSQGCQGCATCSDYNGCLSCKPRLPFVLERIGMKQIGVCLSSCPSGYYGTRYPDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                              (AUTO-) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THIC2 MOUSE STANDARD; PRT; 2470 AA.
035516; Q06008; Q60941;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
88-FEB-2003 (Rel. 41, Last annotation update)
Neurogenic locus notch homolog protein 2 precursor (Notch 2) (Motch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus. Mus.
MCBI_TaxID=10090;
                                                                                                                                                                                       (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 260 C -> S (IN RBF. 2).
301 301 B -> G (IN RBF. 2).
324 324 C -> S (IN RBF. 2).
1134 1134 C -> S (IN RBF. 3).
1145 1144 V -> I (IN RBF. 3).
1145 1145 V -> D (IN RBF. 3).
1137 3A3, 155787 MM; 58B33B72BF101B379 CRC64;
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STRAIN=C57BL/6; TISSUE=Thymus;
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      Best Local Similarity
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MEDLINE=1374376; PubMed=11459941;

Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;

Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;

Conservation of the biochemical mechanisms of signal transduction

among mammalian Notch family members.

E proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).

C Jaggedl, Jaggedz and Deltal to regulate cell-fate determination.

Upon ligand activation through the released notch intracellular

C domain (NICD) it forms a transcriptional activator complex with

RBP-J kappa and activates genes of the enhancer of split locus.

Affects the implementation of differentiation, proliferation and

apoptotic programs (By similarity). May play an essential role in

postimplantation development, probably in some aspect of cell

specification and/or differentiation.

-I- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-

terminal fragment N(BC) which are probably linked by disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=035516-2; Sequence=VSP_001405; Note=No experimental confirmation available; TISSUE SPECIFICITY: Expressed in the brain, liver, kidney, neuroepithelia, somites, optic vesicles and branchial arches, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-95333893; Pubmed-7609614;
Higuchi M., Kiyama H., Hayakawa T., Hamada Y., Tsujimoto Y.;
"Differential expression of Notchl and Notch2 in developing and adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not heart.
DEVELOPMENTAL STAGE: Expressed in the embryonic ventricular zone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Mutation in ankyrin repeats of the mouse Notch2 gene induces early embryonic lethality.";
Development 126:3415-3424(1999).
Hamada Y., Higuchi M., Tsujimoto Y.;
Complete amino acid sequence and mutliform transcripts encoded by
single copy of mouse Notch2 gene.";
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                      Milner L.A., Bigas A., Kopan R., Brashem-Stein C., Bernstein I.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Type I membrane protein. Pollowing proteolytical processing NICD is translocated to the nucleus. ALTERNATIVE PRODUCTS:
                                                                                                     SEGUENCE OF 316-1518 FROM N.A.
STRAIN=C57BL/6 X CBA; TISSUE=Embryo;
MEDLINE=93178563; PubMed=8440332;
Lardelli M., Lendahl U.;
"Motch A and Motch B-two mouse Notch homologues coexpressed in wide variety of tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21523956; PubMed=11518718;
Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;
"Murine notch homologs (N1-4) undergo presenilin-dependent
                                                                                                                                                                                                                                                                                                                                        Martin D.I.;
"Inhibition of granulocytic differentiation by mNotchl.";
Proc. Natl. Acad. Sci. U.S.A. 93:13014-13019(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hamada Y., Kadokawa Y., Okabe M., Ikawa M., Coleman J.R., Tsujimoto Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bvent=Alternative splicing; Named isoforms=2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brain Res. Mol. Brain Res. 29:263-272(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isold=035516-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteolysis.";
J. Biol. Chem. 276:40268-40273(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99396706; PubMed=10393120;
                                                                                                                                                                                                                                                                          SEQUENCE OF 1765-2153 FROM N.A. MEDLINE=97075110; PubMed=8917536;
                                                                                                                                                                                                                                  Exp. Cell Res. 204:364-372(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouse brain.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
the postnatal ependymal cells, and the choroid plexus throughout embryonic and postnatal development.

FTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(BC). Following ligand binding, it is cleaved by TNP-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presentlin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN NOTCH EXTRACELLULAR TRUNCATION.
NOTCH INTRACELLULAR DOMAIN.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor; Transcription regulation; Activator; Differentiation; Developmental protein; Repeat; ANK repeat; BGF-like domain; Transmembrane; Glycoprotein; Signal; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P16109; 1PSB.
MGD; MGI:97364; Notch2.
GO; GO:0005887; C:integral to plasma membrane; IC.
GO; GO:0005515; P:protein binding; IPI.
GO; GO:0002011; P:morphogenesis of an epithelial sheet; IMP.
GO; GO:0007219; P:N signaling pathway; IC.
                                                                                                                                                                                                                                              -!- PTM: Phosphorylated.
-!- SIMILARITY: Belongs to the NOTCH family.
-!- SIMILARITY: Contains 35 BGP-like domains.
-!- SIMILARITY: Contains 2 Lin/Notch repeats.
-!- SIMILARITY: Contains 6 ANK repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE, PS50297; ANK REP REGION; 1. PROSITE; PS50088; ANK REPEAT; 4. PROSITE; PS00010; ASK HYDROXXL; 22. PROSITE; PS00022; EGF 2; 27. PROSITE; PS50026; EGF 2; 27. PROSITE; PS50026; EGF 3; 35. PROSITE; PS01187; EGF CA; 22.
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InterPro; IPR000110; AW.
InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR001431; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR001438; EGF_II.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR008009; Notch.
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Pfam; PF00008; BGF; 34.
Pfam; PF000066; notch; 2.
PIRSF; PIRSF002279; Notch; 1.
PRINTS; PR00011; BGFLAMININ.
PRINTS; PR01452; NOTCH.
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SMART; SM00179; EGF CA; 23.
SMART; SM00004; NL; 3.
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MIC.	EGF-LIKE 2.	EGP-LIKE 4.	Ś	EGP-LIKE 6 ()	BGP-LIKE 7, (	BGP-LIKE 8, (	EGP-LIKE 9, (	EGF-LIKE 10.	EGP-LIKE 11,		EGP-LIKE 13,	-		EGP-LIKE 16,	BGP-LIKE 17,	BGF-LIKE 18,	EGP-LIKE 19.	EGP-LIKE 20,		BGF-LIKE 22.	EGP-LIKE 23,	EGP-LIKE 24,	EGP-LIKE 25,		EGF-LIKE 27,				EGF-LIKE 31,	EGF-LIKE 32,	BGF-LIKE 33.	BGF-LIKE 34.	EGP-LIKE 35.	LIN/NOTCH 1.	LIN/NOTCH 2.	ANK 1.	Score 140.5;
2470	102	180	219	256	294	334	372	411	452	490	528	995	603	641	678	716	753	791	829	869	907	945	983	1021	1059	1097	1145	1183	1221	1260	1300	1345	1410	1454	1533	1869	9.24;
1699	105	144	182	221	258	296	336	373	413	454	492	530	568	605	643	680	718	755	793	831	871	606	947	985	1023	1061	1099	1147	1185	1223	1262	1302	1372	1418	1501	1825	
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Query Match 9.2%; Score 140.5; DB 1; Length 2470; Best Local Similarity 24.4%; Pred. No. 0.026; Matches 54; Conservative 24; Mismatches 56; Indels 87; Gaps 14;

 QY
 30 QRRMHPNVSQCQQCCATCSDVNGCLSCKPRLPFVLERIGMKQIGVCLSSCPSGYYGTRY 89

 DD
 945 QTDMNBCLSBPCKNG-GTCSDYVNSYTC------TCPAGFHGVHC 982

 QY
 90 P-DINKCTKCKVDCDTCFNKNPC-----TKCKSGPYLHLGK 124

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Search completed: June 29, 2004, 17:00:17 Job time: 9.46481 secs

042113 0968P4 080T14 086PQ3 09QVW4 09GQ45 09GQ45 09GXX4

Q91VK0 Q8AY18 Q964D2 O42114 Q9U018

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Q96k87 homo sapien
Q96sb2 mus musculu
Q9cab2 mus musculu
Q9z132 mus musculu
Q9z135 homo sapien
Q9b£u0 mus musculu
Q9ugb2 homo sapien
Q9ugb2 homo sapien
Q9cx homo sapien
Q7cx3 mus musculu
Q8bf33 mus musculu
Q8bf373 mus musculu
Q85489 spodoprera
Q8szs2 drosophila
Q35171 mus musculu
Q8cf22 mus musculu
Q8cf22 mus musculu
                                                                                                                                                                                                                     June 29, 2004, 16:55:24; Search time 35.5522 Seconds (without alignments) 2476.067 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                              1535
1 MHLRLISCPFIILNPMBYIG......QQKRRARDKQQKSVSVSTVH 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1017041
                                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of hits satisfying chosen parameters:
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Q96KB17
Q8EVW2
Q8A132
Q8A715
Q8W7ES
Q8W6ES
Q8W6ES
Q7TPX3
Q8W6X6
Q7TPX3
Q8W6X6
Q7TPX3
Q8W6X6
Q7TPX3
Q8W6X6
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Q8W6X6
Q8W6X6
Q8W6X6
Q8W6X
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Gapop 10.0 , Gapext 0.5
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sp_vertebrate:*
sp_unclassified:*
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sp_mammal:*
sp_mhc:*
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sp_phage:*
sp_plant:*
sp_rodent:*
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sp_bacteria:*
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seq length: 200000000
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sp_human:*
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Maximum DB
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ALIGNMENTS

QBK2QB QBVCC9 QB9UE4 QBRQY1 Q23 B3 2 Q9VCB6 Q9VLCB6 Q9VLXB QB 60 2 QB 60 7 QB

2000	KESULT 1							
36	09BXY4	PRELIMINARY:	PRT	272 AA.				
ğ	09BXY4;							
Ţ	01-JUN-2001	(TrEMBLrel. 17,	Created)					
I	01-JUN-2001	(TrEMBLrel. 17,	Last sequ	Last sequence update)				
DI	01-OCT-2003	(TrEMBLrel. 25,	Last anno	Last annotation update)	(e)			
DR	Thrombospondin	lin.						
SO	Homo sapiens (Human)	(Human).						
႘	Rukaryota; Metazoa;	detazoa; Chordata;	; Craniat	Craniata; Vertebrata; Euteleostomi;	a, Eutele	ostomi	<u>.</u> :	
ဗ	Mammalia, Butheria,		; Catarrh	Catarrhin; Hominidae; Homo.	lae; Homo.			
ŏ	NCBI TaxID=9606;	,606;						
Z	<u>.</u>							
RP	SEQUENCE FROM N.A.							
Æ	Mao Y., Xie Y., Zhou	2.7	o W., Zha	Zhao W., Zhao S., Wang W., Huang Y.,	I., Huang	χ χ.	Wang S.,	
æ	Tang R., Che	ن:						
R	Submitted (MAR-2000)		EMBL/Gent	to the EMBL/GenBank/DDBJ databases	аравев.			
Z	[2]							
RP	SEQUENCE FROM N.A.	M N.A.						
2	TISSUB=Placenta;	enta;						
ð	Strausberg R.;	۲. ;						
R.	Submitted (F	Submitted (FEB-2002) to the	EMBL/GenE	EMBL/GenBank/DDBJ databases	аравев.			
DR	EMBL; AF2510	EMBL; AF251057; AAK34947.1;	;					
S,	EMBL, BC0223	EMBL, BC022367; AAH22367.1;	;					
D.	Genew; HGNC:	Genew; HGNC:20866; THSD2.						
DR	InterPro; IF	InterPro; IPR006212; Furin repeat.	epeat.					
g	InterPro, IP	IPR009030; Grow Fa	Grow Fac recep.					
DR.		IPR000884; TSP1.	ı					
띥	Pfam; PP0009	Pfam; PP00090; tsp 1; 1.						
R	SMART, SM002	SM00261; FU; 2.						
ä	SMART; SM002	SM00209; TSP1; 1.						
留	PROSITE; PS5	PROSITE; PS50092; TSP1; 1.						
8	SEQUENCE 2			CACAEC6B7E781189 CRC64;	RC64;			
5	Query Match		Score 13	Score 1315.5; DB 4;	Length 272;	272;		
ă :	Best Local Similarity	87.18;	Pred. No. 1.8	Pred. No. 1.8e-110;	tadolo	ŀ	920	4
2								r

1 MHLRLISCPFIILNFMEYIGSQNASRGRRQRRMHPNVSQGGQGGCATCSDYNGCLSCKPR 60

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241 GLESSIETPDOQENKEROQQQKRRARDKQQKSVSVS 276
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                                                       61 LPPALERIGHKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYL 120
                                                                                           121 HLGKCLDSCPEGLEANNHTMECVSIVHCEASEWSPWSPCMKKGKTCGFKRGTEFRVRDIL 180
                                                                                                       QHPSAKGKGNLCPPTSETRTCIVQRKKCSKGERGKKGRERKRKKLNKEERKETSSSSDSK 240
                                                                                                                                                           181 QHPSA--KGNLCPPTNETRKCTVQRKKCGRGERGKKGRERKRKKRDNKGESKB--AIPDSK 236
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1 MHLRLISWLFIILINFWEYIGSQNASRGRRQRRWHPNVSQGRQGRQGGATCSDYNGCLSCKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUB-Embryo;

A Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Takahashi-Pujii A., Hara H.,

A Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,

A Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,

Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;

"NEDO human cDNA sequencing project.";

In NEDO human cDNA sequencing project.";

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; AK02746; BABS5051.1;

InterPro; IPR000804; TSPI.

R InterPro; IPR000804; TSPI.

R SMART; SM00261; FU; 2.

R SMART; SM00261; FU; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MHLRLISCPPIILNFWBYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR
                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FL/14440.
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 292;
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Hypothetical protein.
SEQUENCE 292 AA; 33243 MW; 01E2774AC3D4A6F8 CRC64;
                                                                                                                                                                                               241 GLESSIETPDQQENKERQQQQKRRARDKQQKSVSVSTVH 279
                                                                                                                                                                                                              237 SLESSKEIPEQRENK--QQQKQRKVQDK-QKSVSVSTVH 272
                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Rewai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Ra Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fisichmann W., Gasterland T., Gissi C., King B., Kochiwa H.,
Rakai K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Mazzarelli J., Wombaerts P.,
RA Gustincich S., Hill D., Hofmann M., Rodriguez I., Sakamoto N.,
RA Gustincich S., Korchenbach C., Seya T., Shibara Y., Storch K.-F.,
RA Sazaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Rymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Rymshaw-Boris A., Mang K.H., Weitz C., Whittaker C., Wilming L.,
Rymshizaki Y.;
Rymshaw-Boris A., Mang K.H., Weitz C., Whittaker C., Wilming L.,
Rymshizaki Y.;
Rymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Rymshi, Akoli336f, Rabzeslil.;
Rymshi, Rymilade R., Rymshaw-Rall.;
Rymshizaki W.;
Rymshaw-Wall R.,
Rymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Rymsha, Awing R.,
Rymshaw-Boris A., Wang K.H., Weitz C.,
Rymshaw-Wall R.,
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
VCBI_TaxID=10090;
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Pred. No. 3e-101;
....rehes 1; Indels
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237 SLESSKEIPBQRENK--QQQKKRKVQDKQKSGIEVT 270
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InterPro; IPR006212; Furin repeat.
InterPro; IPR006309; Grow_fac_recep.
InterPro; IPR000803; Grow_fac_recep.
InterPro; IPR000804; TSP1.
Pfam; PF00090; tSp_1; 1.
SMART; SM00219; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUB=Embryo;
MEDLINE=21085660; PubMed=11217851;
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Best Local Similarity 98.6%;
Matches 216; Conservative
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InterPro; IPR006212; Furin repeat.
InterPro; IPR009030; Grow Fac_recep.
InterPro; IPR000884; TSP1.
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Matches 112; Conservative
                                                                                                                       Best Local Similarity 43.7
Matches 114; Conservative
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                                                                                                             Query Match
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                                                                                                                                                                                   1 MHLRLISCPFIILNFMBYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kamata T., Katsube K., Michikawa M., Yamada M., Mizusawa H.,
"R-spondin, a novel thrombospondin type 1 domain gene, expressed in
the dorsal neural tube.",
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: AB016768; BAA75640.1; --
                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                72.1%; Score 1107; DB 11; Length 224; BB.4%; Pred. No. 8.7e-92; ative 5; Mismatches 19; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 OHPSAKGKGNLCPPTSBTRTCIVQRKKCSKGERGKKGRERKRKK 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 OHPSA--KGNPVPPNORDKNLYSTKKEVFKGRARKKGKREKTKK 222
                                                                                                                                                                                                                                                                                                                                               SMART; SM00261; FU; 2. SEQUENCE 224 AA; 25398 MW; BC13B083497CFEB3 CRC64;
                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                       InterPro; IPR006212; Furin repeat.
InterPro; IPR009030; Grow_fac_recep.
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                                                                                                                                                                                                                                                                                               EMBL; AK076308; BAC36296.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombospondin type 1 domain. RSPONDIN OR R-SPONDIN.
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                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 88.4
Matches 198; Conservative
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                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                            MGD; MGI:1920030; Thsd2
                                                                                                                          THSD2 OR 2810459H04RIK. Mus musculus (Mouse).
                                                                                                            Thrombospondin homolog
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                                                                                                                                                                          NCBI_TaxID=10090;
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Q9Z132;
                                                            QBBVW2;
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                                                                                                                                                                                                                                                                 181 HAPG--GDHTTCSDTKETRXCTVRATPCPEGGKRRKGGGGRRENANRHPARKNSKEPRS- 237
                                                                                                                                                                                                                                      62 PFVLERIGMKOIGVCLSSCPSGYYGTRYPDINKCTKCKVD-CDTCFNKNFCTKCKSGFYL 120
                                                                                                                                                                                                                                                                                                                                                     121 HIGKCLDSCPEGLEANNHTWRCVSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDIL 180
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                                                                                                                                                     181 OHPSAKGKGNLCPPTSETRTCIVORKKCSKGERGKKGRERKRKGKANKEERKETSSSSDSK
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Oshima A., Takhashi-Pujii A., Tanase T., Imose N., Takeuchi K.,
Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
Otsuki T., Sato H., Wakametu A., Ishii S., Yamamoto J., Isono Y.,
Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
"NEDO human CDNA Sequencing project.";
Submitted (JUL-2002) to the EMBL, GenBank/DDBJ databases.
EMBL; AK098225; BAC05263.1;
                                                                                                                       3 LRLISCFF-IILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRL
                                                              14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaрв
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
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41.2%; Score 632; DB 11; Length 265; 43.7%; Pred. No. 5.8e-49; tive 42; Mismatches 91; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 236 AA; 25942 MW; 8D03803127EC5678 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2002 (TIEMBLEEL. 22, Created)
01-OCT-2002 (TIEMBLEEL. 22, Last sequence update)
01-OCT-2003 (TIEMBLEEL. 25, Last annotation update)
Hypothetical protein FLJ40906.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 AA.
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InterPro; IPR009030; Grow_fac_recep.
InterPro; IPR00884; TSP1.
Pfam, PF00090; tsp_1; 1.
SMRAT; SM00261; FU; 2.
SMRAT; SM00209; TSP1; 1.
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us-09-894-912a-32.rspt

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SEQUENCE
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Matches
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RECORDING CONTROLLUM:

REDING-22356683; PubMed=12466851;

A The FANTOM COMBOTATIUM,

The FANTOM COMBOTATIUM,

The RAINCH COMBOTATIUM,

The RIKEN Genome Exploration Research Group Phase I & II Team;

RT 60,770 full-length CONAS.*;

To 7.70 full-length CONAS.*;

Nature 420:563-573(2002).

REL: AXC049891; BAC33974.1; -..

RENCE : PRO00804; TSP1.

InterPro; IPR000804; TSP1.

SMART; SM00209; TSP1.

REPROSITE: PSS0092; TSP1; 1.

WHYDCHACICAL PROCECUM.

SWART; SM00209; TSP1; 1.

WHYDCHACICAL PROCECUM.

SEQUENCE 243 AA; 28275 MW; ED76A08D61012ED7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 LFFFLRREGMRQYGECLHSCPSGYYGHRAPDMNRCARCRIENCDSCFSKDFCTKCKVGFY 118
                                                                      64 MYKCIKCKIEHCEACPSHNPCTKCKEGLYLHKGRCYPACPEGSSAANGTWECSSPACEV 123
                                                                                                            SEWSPWSPCMCKGKTCGFKRGTETRVRDILQHPSAKGKGNLCPPTSETRTCIVQRKKCSK 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 LHLGKCLDSCPEGLEANNHTMECVSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 LQHPSAKGKGNL-CPPTSETRTCIVQRKKCSKGERGKKGRERKRKKLNKE--ERKETSSS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RMHPNVSQGCQGGCATCSDYNGCLSCKPRLPFVLERIGMKQIGVCLSSCPSGYYGTRYPD 91
                                                                                                                                                                    211 GERGKKG----RERKRKKINKERKGTSSSSDSKGLESSIETPDQQENKERQQQQKR 263
                                                                                                                                                                                   1 MHLRLISCFFIILNFMBYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LFFVLERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKVD-CDTCFNKNFCTKCKSGFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 36.8%; Score 565.5; DB 11; Length 243; Best Local Similarity 45.8%; Pred. No. 5.2e-43; Matches 110; Conservative 36; Mismatches 83; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Sukaryota; Metazoa, Chordata, Craniata; Vertebrata, Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical thrombospondin type I repeat.
2610028P08RIK.
                                                                                                                                                                                                                                                                    243 AA
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RESULT 8

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88 RYPDINKCTKCKVDCDTCFNKNPCTKCKSGPYLHLGKCLDSCPEGLBANNHTMECVSIVH 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 REKKQVGTGLGGRUT-GCIICSEENGCSTCQQRLFLFIRREGIRQYGKCLHDCPPGYFGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 CEASEWSPWSPCMKKGKTCGFKRGTETRVRDI -- LQHPSAKGKGNLCPPTSETRTCIVQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 RRORRMHPNVSQGCQGCCATCSDYNGCLSCKPRLFFVLERIGMKQIGVCLSSCPSGYYGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Gaps
                                                                                                                                                                      Homo sapiens (Human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                      01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DJ824F16.3 (Novel protein similar to mouse thrombospondin type domain protein R-spondin) (Fragment).
DJ824F16.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Match 29.3%; Score 450; DB 4; Length 224; Local Similarity 42.1%; Pred. No. 1.2e-32; les 88; Conservative 33; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                    Blakey S.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, ALOSO1325; CAB65783.3;
Genew; HGNC:16175; C20orf182.
InterPro; IPR006212; Purin repeat.
InterPro; IPR00884; TSP1.
SWART; SM00261; FU; 2.
SWART; SM00261; FU; 2.
SWART; SM0229; TSP1; 1.
PROSITE: PS50027; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC027938; AAH27938.1;
InterPro; IPR006212; Furin repeat.
InterPro; IPR009030; Grow fac_recep.
InterPro; IPR009084; TSP1.
SMART; SM00261; FUU; 1.
SWART; SM00261; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 AA; 25042 MW; 97D26AD34CDBFB12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
224 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 KKCSKGERG---KKGRE----RKRKKLNK 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||| ||||: |||: |||: || 195 P--CPGERSPGOKKGRKORRDRRUDR 221
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similar to putative. Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE PROM N.A. TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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59 LPPFLRREGMRQYGECLHSCPSGYYGHRAPDMNRCARCRIENCDSCFSKDFCTKCKVGFY 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 RRKKQAGTGLGGNCT-GCVICSERNGCSTCQQRLFLFIRREGIRQYGKCVHDCPLGFFGI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Marure 420:563-573(2002).
EMBL; AK020904; BAC25643.1; -...
MGD; MGI:1924467; A930029K19Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa; Arthropoda, Hexapoda; Insecta, Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Ovary;
Cieplik M., Klenk H.;
Cloning and functional characterization of FURIN from Spodoptera "Cloning and functional characterization of FURIN from Spodoptera frugiperda (Sf9) celle.";
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE PAMILY S8.
-!- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Muxinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 11; Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.5%; Score 283.5; DB 11; Length 42.9%; Pred. No. 6.9e-18; Live 23; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00261; FU; 2. _ _ SEQUENCE 138 AA; 15172 MW; FEFD7D949279D5DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q26489;
O-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                       120 LHLGKCLDSCPEGLEANNHTMECVSIVHCEASBWS 154
                                                                                                             119 LHRGRCFDECPDGFAPLDETMECVE--GCEVGHWS
                                                                                                                                                                                                                                                                                                  138 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spodoptera frugiperda (Fall armyworm)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro, IPR006212; Furin repeat.
InterPro, IPR009030; Grow_fac_recep.
                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Noctuidae; Amphipyrinae; Spodoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TYBAIN-CSTBL/60; TISSUE-Retina;
MBDLINE-22354683; PubMed=12466851;
The PANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                   23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45; Conservative
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                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                 Q8BJ73;
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endoprotease furin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4930029K19RIK.
                                                                                                                                                                                                                                                                                                  Q8BJ73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    026489
                                                                                                                                                                                                                                 RESULT 11
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                                                                                                                                                                                                                                                                Q8BJ73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     026489
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                                                                                                                                 셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RX STALINECSTBL/6J; TISSUE=Egg;
RX STALINECSTBL/6J; TISSUE=Egg;
RX STALINE-CSTBL/6J; TISSUE=Egg;
RX Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Lechul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Altechenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.E., Casavant T.L., Scheetz T.B.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Roban S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton B., Kettemen M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Richylez R.W., Touchman J.W., Green E.D., Dickson M.C.,
Richylez R.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rzzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B.,
Razywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B.,
R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                        ŝ
                                                                                                                                                                                                      70 MKQIGVCLSSCPSGYYGTRYPDINKCTKCKVD-CDTCFNKNFCTKCKSGPYLALGKCLDS 128
                                                                                                                                                                                                                                                                                                                                                                                              61 CPDGPAPLEETMECVE -- GCEVGHWSEWGTCSRNNRTCGPKWGLETRTRQIVKKPV---K 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LPFVLERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKVD-CDTCFNKNFCTKCKSGFY 119
                                                                                                                                                                                                                                                                                                                                 CPEGLEANNHIMECVSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDILQHPSAKGK 188
                                                                                                                                                                                                                                    1 MRPCLFSFALITLNCMDYSQCQ-GNRWRRNKRA-SYVSNPICKGCLSCSKDNGCSRCQQK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MHIRLISCFFIILNFWEYIGSQNASRGRRQRRWHPNVSQGCQGGCATCSDYNGCLSCKPR 60
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 GNL-CPPTSETRTCIVQRKKCSKGERGKKGRERKRKKLANKE--ERKETSSS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ņ
                                                                                                                                     9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.3%; Score 419.5; DB 11; Length 152; 51.6%; Pred. No. 4.4e-30; ive 19; Mismatches 51; Indels 5;
                                                                Query Match 29.3%; Score 449.5; DB 4; Length 176; Best Local Similarity 46.8%; Pred. No. 1e-32; Matches 80; Conservative 28; Mismatches 54; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
      20409 MW; OF83CCE1B2F8CA85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2844; AAH52844.1; -.
152 AA; 17658 MW; B74713789B2853R4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-C57BL/6J; TISSUE-Egg;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BC052844; AAH52844.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2610028F08Rik protein.
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   176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 80; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
      SEQUENCE
                                                                                                                                                                                                                                                                                                                                    129
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72; Gaps

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93 NKCTKCKVDCDTCP--NKNPCTKCKSGPYLHLGKCLDSCPEGLEANNHTMECVSIVHCEA 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    745 QFCPDGYFENSRNRTCVPCEPNCASCQDHPEYCTSCDHHLVMHEHKCYSACPLDTYETED 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 SSCPSGYY-----GTRYPDI 92
                                                                                                                                                                                                                                                                                                                                                                                            23 NASRGRRORRMHPN -- - VSQGCQGCCATCSDY -- NGCLSCKPRLPFVLBRIGMKQIGVCL
                                                                                                                                                                                                                                                                                                         Query Match 11.3%; Score 174; DB 5; Length 1376; Best Local Similarity 24.5%; Pred. No. 5.2e-07; Matches 48; Conservative 15; Mismatches 61; Indels 7;
                                                    | Pfam; PP00182; Peptidase SB; 1. |
| Pfam; PP00183; Peptidase SB; 1. |
| Pfam; PP01483; P_proprotein; 1. |
| PRINTS; PR00723; SUBTILISIN. |
| ProDom; PD00071; Pu; 10. |
| PROSITE; PS00190; CYTOCHROME C; 3. |
| PROSITE; PS00137; SUBTILASE ASP; 1. |
| PROSITE; PS00137; SUBTILASE HIS; 1. |
| PROSITE; PS00138; SUBTILASE SRE; 1. |
| PROSITE; PS00138; SUBTILASE SRE; 1. |
| PROSITE; PR00138; SUBTILASE SRE; 1. |
| PROSITE; PS00138; SORTINE SRE; 1. |
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InterPro; IPR009030; Grow Fac_recep.
InterPro; IPR007030; IRGF.
InterPro; IPR007087; Znf_C2H2.
SWART; SM00181; BGF; 2.
SWART; SM00261; FU; 5.
PROSTIE; PS00028; ZINC_PINGER_C2H2_1; 1.
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interPro; IPR009030; Grow fac_recep
InterPro; IPR000209; Peptidase_SB.
InterPro; IPR002884; Peptidase_SBB.
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| 858 -----PCQEGCKTC 866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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PCSK6 OR PACE4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 NVSQGCQGGCATCSD-YNGCLSCKPRLFFVLERIGMKQIGVCLSSCPSGYYGTRYPDINK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise B.,
George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.B., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     904 TSAFCLSCEPKWELNKKGKCMPVGSDKCSAGBFAVDQKCKRCNPACDSCYGEN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63;
                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 12.1%; Score 185.5; DB 5; Length 1299; 1 Similarity 24.5%; Pred. No. 4.6e-08; 54; Conservative 24; Mismatches 79; Indels 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterayera; Endopterygota; Diptera; Brachycera; Muscomorpha; Bphydroida; Drosophilidae; Drosophila.
          HISP; 099405; 1M251.

R GO; GO:0008233; F:peptidase activity; IEA.

GO; GO:0008233; F:peptidase activity; IEA.

GO; GO:0008289; F:subtilase activity; IEA.

GO; GO:0006289; F:subtilase activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR002021; Purin repeat.

InterPro; IPR002039; Peptidase SBB.

InterPro; IPR00284; Peptidase SBB.

InterPro; IPR002020; Protease Inhib.

Pram; Pr004082; Peptidase SBB.

R Pfam; Pr01483; P:proprotein; 1.

R Pfam; Pr01483; P:proprotein; 1.

R PRNTS; PR00723; SUBTILISIN.

R PRNSITE; PS00136; SUBTILASE ASP; 1.

R PROSITE; PS00136; SUBTILASE HIS; 1.

R PROSITE; PS00138; SUBTILASE SER; 1.

HYdrolase; Protease; Serine protease.

SEQUENCE 1299 AA; 142020 MW; 4C3799C7BBC572AB CRC64;
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Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
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WEDLINE-98053888; PubMed-9393739;
Hubbard F.C., Goodrow T.L., Liu S.C., Brilliant M.H., Basset P.,
Hubbard R.C., Goodrow T.L., Liu S.C., Brilliant M.H., Basset P.,
Mains R.E., Klein-Szanto A.J.;
Wains R.E., Klein-Szanto A.J.;
With spindle cell tumor conversion and increased invasive ability.";
Cancer Res. 57:5226-5231(1997).
EMBL; AP008222; AAB95315.1; -.
MGD; MGI:102897; Pacc4.
                                                                          Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.1%; Score 171; DB 11; Length 296; 22.9%; Pred. No. 2e-07;
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Last sequence update)
Last annotation update)
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RESULT 13
088282
AC 088282
AC 088282
DT 01-JU
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                                                            64 YPGDAAARRCRR-----CHKGCETCTGRSPAQCLSCR-RGFY----HHQETNT 106
                                                                                                                 76 CLSSCPSGYYGTRYPDINKCTKCKVDCDTCPNK-NPCTKCKSGPYLHLGKCLDSCPRGLB 134
                                                                                                                                      135 ANNHIMEC-----PWSP 158
                                                                                                                                                                                                                       165 PDSELVKCGECHHTCRTCVGPSREECIHCAKSFHPQDWKCVPACGEGFYPEEMPGLPHKV 224
                                                                                                                                                                                                                                                                          159 CMKKGKTC----GFKRG-----TETRVRDILQHPSAKGKGNLCPPTSETRTCIVQRK 206
                                                                                                                                                                                                                                                                                                              225 CRRCBENCLSCEGSSRNCSRCKAGFTQLGTSCITNHTCSNADETFCEMVKSNRLC--ERK 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 CLSSCPSGYYGTRYPDINKCTKCKVDCDTCPNK-NPCTKCKSGFYLHLGKCLDSCPRGLR 134
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                                      18 YIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYN--GCLSCKPRLFFVLERIGMKQIGV 75
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72; Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.1%; Score 171; DB 11; Length 826; Best Local Similarity 22.9%; Pred. No. 5.8e-07; Matches 55; Conservative 25; Mismatches 88; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberger R.;
Strausberger R.;
Strausberger R.;
Submitted (SEP-2002) to the EWBL/GenBank/DDBJ databases.
BMBL; BC031450, AAH37450.1;
GG; GO:0005489; F:electron transporter activity; IEA.
GG; GO:00064289; F:electron transport; IEA.
GG; GO:0006189; P:electron transport; IEA.
GG; GO:0006189; P:electron transport; IEA.
GG; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000340; Cytc.heme.BS.
InterPro; IPR000212; Purin repeat.
InterPro; IPR000212; Purin repeat.
InterPro; IPR000209; Peptidase.S8.
InterPro; IPR000209; Peptidase.S8.
InterPro; IPR000209; Peptidase.S8.
InterPro; IPR000209; Peptidase.S8.
InterPro; IPR00082; Peptidase.S8.
InterPro; IPR00082; Peptidase.S8:
InterPro; IPR00082; Peptidase.S8:
IPEan; PP00482; Peptidase.S8:
IPEan; PP00483; Proprotein:
REMITS; RN00181; RGF; S.
SWART; SW00181; RGF; S.
88; Indels
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826 AA; 91653 MW; 61BC6B49F6F42AA0 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to subtilisin-like endoprotease (Fragment).
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  25; Mismatches
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PROSITE; PS00136; SUBTILASE_ASP; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
PROSITE; PS00028; ZINC_FINGER_CZH2_1; 1.
  55; Conservative
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  Matches
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159 CMKKKKTC----GPKKG-----TETRVRDILQHPSAKGKKMLCPPTSETRTCIVQRK 206
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Search completed: June 29, 2004, 17:02:18 Job time : 41.5522 secs

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inflammation disease
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N-PSDB; AAH45131.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                  OM protein - protein search, using sw model
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AAE13168
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Maximum DB seq length: 200000000
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## ALIGNMENTS

Human; thrombospondin-30; cytostatic; anti-HIV; antiinflammatory; malignant tumour; haemopathy; HIV infection; immunological disease; (BIOR-) BIOROAD GENE DEV LTD SHANGHAI. AAB99220 standard; protein; 272 AA 27-NOV-2000; 2000WO-CN000494. 29-NOV-1999; 99CN-00124148 (first entry) Human thrombospondin-30.

Human thrombospondin-30 and polynuclectide is useful in diagnosis and treatment of, e.g., malignant tumor, hemopathy, HIV infection, immunological diseases and various inflammatory diseases.

Claim 1; Page 27-28; 33pp; Chinese.

The present sequence is the protein sequence for human thrombospondin-30. Thrombospondin-30 protein and coding sequence are useful in the diagnosis and treatment of mailgnant tumour. haemopathy, HIV infection, immunological diseases and various inflammation diseases. In addition thrombospondin-30 protein may be used for screening mimics, agonists, antagonists or inhibitors, or for use in peptide fingerprinting identification. The thrombospondin-30 coding sequence may be used as primers for nucleic acid amplification reaction or as probes for hybridisation reaction, or in producing gene chips or microarrays

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, Chen R, Wang ZW;
                                                                                                                    1 MHLRLISWLFIILNFWEYIGSQNASRGRRQRRMHPNVSQGCQGCCATCSDYNGCLSCKPR
                                                                                                                                                         MILRLISWLFIILNFWEYIGSONASRGRRORRMEPNVSOGCOGGCATCSDYNGCLSCKPR
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                                                                ö
      Length 272;
                                                                Indels
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Wang J, Zhang J, Ren F,
n T, Goodrich R;
      DB 4;
100.0%; Score 1510; DB 4;
100.0%; Pred. No. 1e-110;
ive 0; Mismatches 0;
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20-JUN-2000; 2000US-00598075.
19-JUL-2000; 2000US-00654936.
01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-00653551.
20-OCT-2000; 2000US-0063325.
30-NOV-2000; 2000US-00584325.
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Ma Y, Zhao QA, Wang D, Wang
Xue AJ, Yang Y, Wejhrman T,
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                              Best Local Similarity 100.
Matches 272; Conservative
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      Query Match
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encoded polypeptides (AAMY8323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAKS2SB1), 2111 (AAKS2SB2) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
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                                                                                                                                                                                                                                                                                                                                                                                                                    MHLRLISWLFIILLNFWEYIGSQNASRGRRQRRWHPINVSQGCQGGCATCSDYNGCLSCKPR
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/label= Signal peptide
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Matches 272; Conservative
                                                                                                                                                                                                                                                                           Sequence 272 AA;
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Peptide
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The patent discloses novel stem cell growth factor-like proteins and polymucleotides encoding them. Proteins of the invention are also known as supporting factor for the proliferation of stem cells (SCR-1). Stem cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell or germ cell which is preferably primordial germ cell, germ line stem cell, embryonic stem cell, haematopoietic stem cell, haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell cultured using stem cell growth factor-like proteins can replace as a graft for the bone marrow transplantation or cord blood transplantation for treating a variety of diseases such as immunodeficiency syndrome, chronic granulomatous
                                                                                                                                                                                                                                                                                                                                    Novel stem cell growth factor like polypeptides and polynucleotides for identifying modulators useful for treating diseases such as Alzheimer's disease, cancer, rheumatoid arthritis, osteoporosis.
                                                                                                                                                                                                                                  Tang TY, Labat I, Tillinghast JS, Sinku A, Liu C,
Stache-Crain B, Dickson M, Mize NK, Nishikawa M;
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 28; Page 226-227; 232pp; English
                                                                                                               28-JUN-2000; 2000US-0215733P.
09-JAN-2001; 2001US-00757562.
05-FEB-2001; 2001US-0266614P.
                                                                05-APR-2001; 2001WO-US011208.
                                                                                                 2000US-00543774
                                                                                                                                                                                (HYSE-) HYSEQ INC.
(KIRI ) KIRIN BEER KK.
                                                                                                                                                                                                                                                                                 WPI; 2001-657166/75.
N-PSDB; AAD21728.
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WO200177169-A2
                                                                                                 05-APR-2000;
                                 18-OCT-2001
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Drmanac RT;

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disease, duplicated immunodeficiency syndrome, agammaglobulinaemia, wiskott-Aldrich syndrome, acquired immune deficiency syndrome (AIDS), thalassaemia, haemolytic anaemia due to enzyme defect, congenital anaemia such as sickle cell anaemia, Gaucher's disease, lysosomal storage diseases such as mucopolysaccharidosis, adrenal white matter degeneration, a variety of cancer and tumours. Proteins of the invention are useful for treating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, thrombocytopaenia, immune deficiencies and disorders such as severe combined immunodeficiency
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                                                                                                                                                                                                                                                                                                                                         (SCID)) and autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, and autoimmune pulmonary
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The patent discloses novel stem cell growth factor-like proteins and polynucleotides encoding them. Proteins of the invention are also known as supporting factor for the proliferation of stem cells (SCR-1). Stem cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell or germ cell which is preferably primordial germ cell, germ line stem cell, embryonic stem cell, haematopoietic stem cell, haematopoietic progenitor cell, puripotent cell or totipotent cell. The haematopoietic progenitor cell cultured using stem cell growth factor-like proteins can replace as a graft for the bone marrow

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Human; stem cell growth factor-like protein; antiinflammatory; nootropic;
                                                                                                                                                                                                                                 neuroprotective; vulnerary; cytostatic; anticonvulsant; immunostimulant; vasotropic; virucide; dermatological; tranquilliser; cerebroprotective; osteopathic; immunodeficiency syndrome; chronic granulomatous disease; duplicated immunodeficiency syndrome; Wischtorlandrich syndrome; AlbB; acquired immunodeficiency syndrome; Masclobulinaemia; thalassaemia; Gaucher's disease; lysosomal storage disease; mucopolysaccharidosis;
                                                                                                                                                                                                                                                                                                                        adrenal white matter degeneration; anaemia; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; thrombocytopaenia; SCID; severe combined immunodeficiency; immune disorder; autorimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; autoimmune pulmonary inflammation; cancer; tumour; gene therapy; SCR-1; supporting factor for the proliferation of stem cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel stem cell growth factor like polypeptides and polynucleotides for identifying modulators useful for treating diseases such as Alzheimer's disease, cancer, rheumatoid arthritis, osteoporosis.
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Nishikawa M;
                                                                                                                                                                                        Human stem cell growth factor-like protein #2.
             241 SKBIPBQRENKQQQKKRKVQDKQKSVSVSTVH 272
241 SKRIPRORENKOOOKKRKVODKOKSVSVSTVH 272
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/label= Signal_peptide
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                                                                                                   AAB13150 standard; protein; 272
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28-UNW-2000; 2000US-0215733P.
09-JAN-2001; 2001US-00557562.
05-FRB-2001; 2001US-0266614P.
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Stache-Crain B, Dickson M,
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BEER KK.
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N-PSDB; AAD21724.
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(KIRI ) KIRIN
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                                                                                                                               AAB13150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
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                                                                                      AAB13150
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transplantation or cord blood transplantation for treating a variety of diseases such as immunodeficiency syndrome, chronic granulomatous clienaes, duplicated immunodeficiency syndrome, agammaglobulinaemia, wiskort.Aldrich syndrome, acquired immuno deficiency syndrome (AIDS), thalassaemia, haemolytic anaemia due to enzyme defect, congenital anaemia cuch as sickle cell anaemia, Gaucher's disease, lysosomal storage diseases such as mucopolysaccharidosis, adrenal white matter degeneration, a variety of cancer and tumours. Proteins of the invention crate useful for treating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, thrombocytopaenia, immune cate and other neurodegenerative diseases, thrombocytopaenia, immune deficiencies and disorders such as sultiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, and autoimmune pulmonary inflammation. Sequences of the invention are also useful in gene therapy.

The present sequence is stem cell growth factor-like protein from human
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                                                                                                                                                                                                                                                                                                                                                                                                                               1 MHLRLISWLPIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGCCATCSDYNGCLSCKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; secreted; stem cell growth factor; cytostatic; haemostatic; neuroprotective; immunostimulant; leukaemia; haemophilia; cancer; degenerative disease; Alzheimer's disease; food supplement;
                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1510; DB 4; Length 272; 100.0%; Pred. No. 1e-110; ive 0; Mismatches 0; Indels 0
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10-DEC-2001; 2001US-0339739P.
19-APR-2002; 2002US-00125852.
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                                                                                                                                                                                                                                                                                                              Sequence 272 AA;
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ABR62112
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The invention relates to new stem cell growth factor-like polypeptides and polynucleotides. The stem cell growth factor-like polypeptides and polynucleotides are useful for inducing differentiation of embryonic and adult stem cells to give rise to different cell types, for treating e.g. cannit stem cells to give rise to different cell types, for treating e.g. leukaemia, haemophilia and degenerative diseases like Alzheimer's compared to the polynucleotides are set of disease. They are also useful for generating one tissues and organs that compared to a partial as hybridisation probes, oligomers or primers for PCR, for useful as hybridisation probes, oligomers or primers for PCR, for chromosome and gene mapping, in recombinantly producing protein, in comparating antisense DNA or RNA, in diagnostics as expressed sequence tags for identifying expressed genes, and for inducing immune response. The polypeptides are useful for generating antibodies that specifically bind the polypeptide, as molecular weight markers, and as a food supplement (e.g. protein or amino acid supplement, and as a carbon, nitrogen or carbohydrate source). Compositions comprising the current cor prevention of cancers, and other immunological disorders. The current expensents a human clone I thrombospondin protein
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                                                            useful
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                                                          New stem cell growth factor-like polypeptides and polynucleotides, use for treating e.g. leukemia, hemophilia and degenerative diseases like Alzheimer's disease, and for inducing immune response.
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                                                                                                                                                      Disclosure; Fig 1; 151pp; English.
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Best Local Similarity 100.0%;
Matches 272; Conservative 0;
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ABO44432
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The invention relates to an isolated stem cell growth factor-like polypeptide (referred as supporting factor for proliferation of stem cells (SCR-1)) from mouse or human, or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity. Also included are an isolated polymucleotide encoding SCR-1 for its mature protein portion, or fragment, analogue, variant or scrivity. Also included are an isolated polymucleotide encoding CSCR-1 polymucleotide, a polymucleotide, and stem contain the SCR-1 polymucleotide, a most cell growth a regulatory sequence CSCR-1 polymucleotide in operative association with a regulatory sequence CSCR-1 polymucleotide in operative association with a regulatory sequence CSCR-1 polymucleotide in polypeptide which is an controls expression product of the polymucleotide (the polypeptide which is an contivity to support proliferation or survival of haematopoietic stem cell comparise the as sequence appearing as ABCA4433), and contained and sequence does not comparise the as sequence appearing any 10 consecutive as from ABCA4430, an isolated polypeptide on an an abcarage of lacking any 10 consecutive as from ABCA4430, an isolated polypeptide comparise the sequence comprising the SCR-1 polymucleotide or a unique segment of the SCR-1 polymucleotide or a unique segment of the SCR-1 polymucleotide or a unique segment of polypeptide attached to a surface, a stromal cell genetically engineered to express the SCR-1 polymucleotide or a unique segment of polymetically engineered to express the SCR-1 polymucleotide or a unique segment of polymetically engineered to express the SCR-1 polymothedicide or a unique segment of polymetically engineered to express the SCR-1 polymothedicide or a unique segment of polymetically engineered to express the SCR-1 polymothedicide or a unique segment of the SCR-1 polymothedic attached to a surface, a strome cell or gene cell
                                                                                                                                                                                   /note= "Mature stem cell growth factor-like protein. This protein is specifically claimed in claim 9°
epithelial cell growth; ovarian follicle development; nerve cell growth; cartilage remodeling; bone growth; immunosuppression; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated polypeptide having stem cell growth factor activity, useful for promoting wound healing, and as a medicine to proliferate or support human hematopoietic stem cells or human hematopoietic progenitox
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                                                                                                                          1. .21
/label=_Signal_peptide
                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 23; Page 82; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                        28-JUN-2000; 2000US-0215733P.
05-FEB-2001; 2001US-0266614P.
05-APR-2001; 2001US-0282397P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LABAT I.
DRMANAC R T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIZE N.
NISHIKAWA M.
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                                                                                                                    Peptide
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healing. The human haematopoietic stem cell or human haematopoietic progenitor cell culture using the SCR-1 polypeptide can replace as a graft for the conventional bone marrow transplantation or cord blood transplantation. The transplantation of haematopoietic stem cells can be employed as a therapy for treating diseases such as chronic granulomatous diseases, duplicated immunodeficiency syndrome, agammaglobulinaemia, wiskott-Aldrich syndrome, ALDS, etc., thalassaemia, haemolytic anaemia due to enzyme defect, congenital anaemia such as sicklaemia, Gaucher's disease etc. the SCR-1 polypeptide is useful for cell growth and morphogenesis, including tissue specific stem cell growth, epithelial cell growth, sustaining neuronal populations, cartilage remodeling, bone growth, and immunosuppression. The present sequence is a Human SCR-1
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                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1510; DB 6; Length 272; 100.0%; Pred. No. 1e-110; ive 0; Mismatches 0; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                           Matches 272; Conservative
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                 Sequence 272 AA;
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Chao C;

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05-APR-2001; 2001US-0282397P
                         N-PSDB; ACH04323, ACH04324.
      LABAT I.
DRMANAC R T.
          MIZE N.
NISHIKAWA M.
                       WPI; 2003-625403/59
                   Labat I,
              CHAO C.
                  Fang YT,
          (MIZE/)
(NISH/)
              (CHAO)
      LABA
        DRMA/
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                                                                                                                                       The invention relates to an isolated stem cell growth factor-like polyperide (referred as supporting factor for proliferation of stem cells (SCR-1) from mouse or human, or its mature protein portion, or tragement, analogue, variant or carrivative, that retains stem cell growth factor activity. Also included are an isolated polymucleotide encoding SCR-1 (or its mature protein portion or fragement, analogue, variant or carrivative, that retains stem cell growth factor activity or the complement of the polymucleotide, a host cell growth factor activity or the complement of the polymucleotide, a host cell growth factor activity or the complement of the polymucleotide, a polypeptide or comprising the SCR-1 polymethed or carrivation with a regulatory sequence or comprision of the SCR-1 polymethed. A provise that controls expression of the SCR-1 polymethed with a provise that controls expression of the SCR-1 polymethed with a provise that controls expression product of the SCR-1 polymethed with a provise that cereminate and activity to support proliferation or survival of basentopoietic stem of activity and activity and activity and activity to support proliferation or survival of or promore proliferation of a stem consolated soft and an analogue or hasmatopoietic progenies the as from ABO44430, an isolated polypeptide with stem cell growth factor activity baving at least an as a sequence appearing as ABO44430, an isolated polypeptide consolativity of or actoric paninal survival of or promore proliferation of a stem cell or germ cell and an implant comprising the SCR-1 polymethed to surpore proliferation or centraling the SCR-1 polymethed as attached to express the SCR-1 polypeptide to support proliferation or survival of a stem cell or germ cell and an implant comprising or cell or germ cell and an implant comprising or cell or germ cell and an implant or survival of a stem cell or germ cell and an implant or survival of a stem cell or germ cell and an implant or cell certain or survival of a stem cell or germ cell a
                                                                                   Claim 23; Fig 3; 96pp; English.
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Drmanac RT;

Claim 28; Page 214-215; 232pp; English

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Gaps

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Human; stem cell growth factor-like protein; antiinflammatory; nootropic; neuroprotective; vulnerary; cytostatic; anticonvulsant; immunostimulant; vasotropic; virucide; dermatological; tranquilliaer; cerebroprotective; osteopathic; immunodeficiency syndrome; chronic granulomatous disease; duplicated immunodeficiency syndrome; wiskott-Aldrich syndrome; AIDS; acquired immunodeficiency syndrome; agammaglobulinaemia; thalassaemia; Gaucher's disease; passenderinaemia; thalassaemia; adrenal white matter degeneration; anaemia; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; thrombocytopaenia; SCID; severe combined immunodeficiency; immune disorder; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; autoimmune pulmonary inflammation; cancer; tumour; gene therapy; SCR-1; supporting factor for the proliferation of stem cell.
                                                                                                                                                                                                    121 HLGKCLDNCPEGLEANNHTWECVSIVHCEVSEWNPWSPCTKKGKTCGPKRGTETRVREII 180
                                                                                                                                                                                                                                                                                       191 QHPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKRDNKGESKEAIPDSKSLES 240
                                                                                                          61 LPFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNRNPCTKCKSGFYL 120
                                                                                                                                                                                                                                                                QHPSAKGNLCPPTNETRKCTVQRKKCQKGBRGKKGRBRKRKKPNKGBSKBAIPDSKSLBS 240
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                         1 MHLRLISWLFIIILMFWEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR
MHLRLISWLFIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGCCATCSDYNGCLSCKPR
                                                                                       61 LPPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYL
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ckson M, Mize NK, Nishikawa M;
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                                                                                                                                                                                                                                                                                                                                                      241 SKEIPBQRENKQQQKKRKVQDKQKSVSVSTVH 272
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28-JUN-2000; 2000US-0215733P.
09-JAN-2001; 2001US-00757562.
05-FEB-2001; 2001US-0266614P.
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Stache-Crain B, Dickson M,
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                                                                                                                                                                                                                                                                                 Novel isolated polypeptide having stem cell growth factor activity, useful for promoting wound healing, and as a medicine to proliferate or support human hematopoietic stem cells or human hematopoietic progenitor cells
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                                                                                                                                                                             Drmanac RT, Mize N, Nishikawa M,
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Homo sapiens.

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The patent discloses novel stem cell growth factor-like proteins and polymucleotides encoding them. Proteins of the invention are also known as supporting factor for the proliferation of stem cells (SCR-1). Stem cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell, embryonic stem cell, paramatopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell pluripotent cell growth cell. The haematopoietic progenitor cell pluripotent cell growth cell. The haematopoietic progenitor cell cultured using stem cell growth cell. The haematopoietic progenitor cell cultured using stem cell growth cell. The haematopoietic progenitor cell cultured using stem cell growth cell can replace as a graft for the bone marrow cell diseases such as immunodeficiency syndrome, chronic granulomatous diseases, duplicated immunodeficiency syndrome, agammaglobulinaemia, wiskott-Aldrich syndrome, acquired immuno deficiency syndrome (AIDS) chalassemia, haemolytic anaemia due to enzyme defect, congenital anaemia cell seases such as sickle cell anaemia (Gaucher's disease, lysosomal storage degeneration, a variety of cancer and tumours. Proteins of the invention cell are useful for treating diseases such as Parkinson's disease, Alzheimer's immunos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SCID)) and autoimmune disorders such as multiple sclerosis, systemic upus erythematosus, rheumatoid arthritis, and autoimmune pulmonary inflammation. Sequences of the invention are also useful in gene therapy. The present sequence is stem cell growth factor-like protein from human
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Sequence 273 AA;

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                                                                                                              3 HIRLISWLFIIILNFWEYIGSQNASRGRRQRRWHPNVSQGCQGGCATCSDYNGCLSCKPRL
                                                                                    2 HLRLISWLFIILNFWEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRL
                                                                                                                                                                     62 FPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLH
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                                               Gaps
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99.7%; Score 1505; DB 4; Length 273; 100.0%; Pred. No. 2.5e-110; ive 0; Mismatches 0; Indels 0
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Human stem cell growth factor-like protein, SCR 1 #2. ABO44414 standard; protein; 273 AA 30-SEP-2003 (first entry) RESULT 9 AB044414 

Stem cell growth factor-like protein; antianemic; anti-HIV; SCR-1; immunostimulant; vulnerary; haematopoietic stem cell; gene therapy; bapporting factor for proliferation of stem cells; wound healing; haematopoietic progenitor cell; stromal cell; AIDS; thalassaemia; bone marrow transplantation; cord blood transplantation; chronic granulomatous disease; duplicated immunodeficiency syndrome; agammaglobulinemia; wiskott-Aldrich syndrome; haemolytic anaemia; congenital anaemia; sicklaemia; Gaucher's disease; morphogenesis; epithelial cell growth; ovarian follicle development; nerve cell growth; cartilage remodeling; bone growth; immunosuppression; human.

Tang YI, Labat I, Drmanac RT, Mize N, Nishikawa M, 28-JUN-2001; 2001US-00894912. 05-FEB-2001; 2001US-0266614P. 2000US-0215733P. DRMANAC R T. MIZE N. NISHIKAWA M. WPI; 2003-625403/59. TANG Y T. N-PSDB; ACH04325 LABAT I. US2003044792-A1 CHAO C. 28-JUN-2000; 06-MAR-2003. (NISH/) (CHAO/) (TANG/) (MIZB/) LABA/ DRMA/ 

Chao C;

The invention relates to an isolated stem cell growth factor-like polypeptide (Ireferred as supporting factor for proliferation of stem coll growth call (GEGT-1)) from mouse or human, or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity. Or the chartwative, that retains stem cell growth factor activity, or the derivative bat retains stem cell growth factor activity, or the carrial stem cell growth factor activity, or the strength of the polyuncleotide, a host cell genetically empiresed to contain the comport proparation of the SCR-1 polymentectide in operative association with a regulatory sequence that controls expression of the polymelectide that he having an expression product of the SCR-1 polymented that a proviso that Cell, not preparation of the SCR-1 polymented or survival of the comport proliferation or survival of the comport proliferation or survival of contained scR-1 polymented as sequence appearing as ABG44438 and ABG44438 and ABG44439, a culture medium comprising the SCR-1 polymented contained and the scr-1 polymented or activity having at least an as sequence appearing as ABG44438 and ABG44439, a culture medium comprising the SCR-1 polymented contained to maintain survival of or promote proliferation or survival of sem cell or germ cell, and an implant comprising the SCR-1 polymented to surface, a strong conting and the SCR-1 polymented to support proliferation or survival of a sem cell or germ cell or germ cell or germ cell or germ cell or a surface, a strong cell call or a surface, a strong conting and contained to express the SCR-1 polymented call or support proliferation or survival of a sem cell or germ cell or germ cell or a surface, a strong cell or germ cell or germ cell or germ cell or a surface, a strong cell or germ cell or a surface, a strong cell or a surface, a strong c Novel isolated polypeptide having stem cell growth factor activity, useful for promoting wound healing, and as a medicine to proliferate or support human hematopoietic stem cells or human hematopoietic progenitor Claim 23; Page 72-73; 96pp; English.

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morphogenesis, including tissue specific stem cell growth, epithelial cell growth and regulation, ovarian follicle development, promoting nerve cell growth, sustaining neuronal populations, cartilage remodeling, bone growth and immunosuppression. The present sequence is a Human SCR-1
                                                                                                                                                                                                                                                                             FPALERIGHKOIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCPNKNFCTKCKSGFYLH 122
                                                                                                                                                                                                                                                                                                                                         LGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQ 181
                                                                                                                                                                                                                                                                                                                                                                                        HPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGESKEAIPDSKSLESS 241
                                                                                                                                                                                                                                                          FFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stem cell growth factor-like protein; antiinflammatory; nootropic;
                                                                                                                                                                                                              HLRLISWLFIILNFWEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRL 62
                                                                                                                                                                                            2 HLRLISWLFIILNPMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuroprotective; vilnerary; cytostatic; anticonvulsant; imminotinulary; vasotropic; virucide; dermatological; tranquilliser; cerebroprotective; ossteopethic; immunodeficiency syndrome; chronic granulomatous disease; duplicated immunodeficiency syndrome; wiskott-Aldrich syndrome; Albis, acquired immunodeficiency syndrome; wiskott-Aldrich syndrome; halbs; acquired immunodeficiency syndrome; wiskott-Aldrich syndrome; halbs; adveher's disease; lysosomal storage disease; mucopolysaccharidosis; advenel white matter degeneration; all mucopolysaccharidosis; parkinson's disease; Alzheimer's disease; thrombocytopaenta; SCID; multiple sclerosis; systemic lugue srythematosus; rheumatoid arthritis; autoimmune pulmonary inflammation; cancer; tumour; gene therapy; SCR-1; supporting factor for the proliferation of stem cell; secreted protein.
                                                                                                                                                              Gape
                                                                                                                                                            ö
                                                                                                                            Length 273;
                                                                                                                                                            0; Indels
                                                                                                                              Score 1505; DB 6; L
Pred. No. 2.5e-110;
                                                                                                                99.7%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEI PEQRENKQQQKKRKVQDKQKSVSVSTVH 272
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28-JUN-2000; 2000US-0215733P.
09-JAN-2001; 2001US-0075562.
05-PEB-2001; 2001US-0266614P.
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                                                                                                                                                            Matches 271; Conservative
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                                                                                                                          Query Match
Best Local Similarity
                                                                                                 Sequence 273 AA;
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KIRIN
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(KIRI )
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The particulations in the control of the invention are also known as supporting factor for the proliferation of stem cells (SCR-1). Stem cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell or germ cell which is preferably primordial germ cell, germ line stem cell, embryonic stem cell, haematopoietic stem cell, haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, cell or totipotent cell. The haematopoietic progenitor cell. The bone marrow cell canappantation or cord blood transplantation for treating a variety of disease, duplicated immunodeficiency syndrome, chronic granulomatous disease, duplicated immunodeficiency syndrome, agammaglobulinaemia, wiskott-Aldrich syndrome, acquired immune deficiency syndrome (AIDS). Thalsassemia, haemolytic anaemia due to enzyme defect, congenital anaemia cuch as sickle cell anaemia, Gaucher's disease, lysosomal storage degeneration, a variety of cancer and tumours. Proteins of the invention are useful for treating diseases such as Barkinson's disease, Alzheimer's deficiencies and other neurodegenerative diseases, thrombocytopaenia, immune deficiency control of the control of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SCID)) and autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, and autoimmune pulmonary inflammation. Sequences of the invention are also useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                            Novel stem cell growth factor like polypeptides and polynucleotides for identifying modulators useful for treating diseases such as Alzheimer's disease, cancer, rheumatoid arthritis, osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MELRISWLFIILNFMEYIGSQNASRGRRQRRMHPNVSQCQGGCATCSDYMGCLSCKPR
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                                                                                                                                                                                                                                                                        patent discloses novel stem cell growth factor-like proteins and
RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is human secreted protein from clone DA228_6
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Drmanac
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Liu C,
Sinku A, Liu
Nishikawa M;
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Labat I, Tillinghast JS, S.
In B, Dickson M, Mize NK,
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                                                                                                                                                                                                                       Disclosure; Fig 3; 232pp; English.
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Best Local Similarity 100.0
Matches 265; Conservative
                                                                        WPI; 2001-657166/75.
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immunostimulant; vulnerary; haematopoietic stem cell; gene therapy; immunostimulant; vulnerary; haematopoietic stem cells; wound healing; haematopoietic progenitor cell; stromal cell; halbs; thalassaemia; bone marrow transplantation; cord blood transplantation; chronic granulomatous disease; duplicated immunodeficiency syndrome; agammaglobulinaemia; Miskott-Aldrich syndrome; haemolytic anaemia; congenital anaemia; sicklaemia; gaucher; sisease; morphogenesis; epithelial cell growth; ovarian follicle development; nerve cell growth; cartilage remodeling; bone growth; immunosuppression; human. cell growth factor-like protein; antianemic; anti-HIV; SCR-1;

Homo sapiens

US2003044792-A1

06-MAR-2003

28-JUN-2001; 2001US-00894912

28-JUN-2000; 2000US-0215733P.

05-PEB-2001; 2001US-0266614P.

LABAT I. DRMANAC R T. TANG Y T. MIZE N. (MIZE/) (NISH/) (TANG/) (LABA/) (DRMA/)

NISHIKAWA M.

CHAO C.

CHINO/

Nishikawa M, Mize N, Drmanac RT, Fang YT, Labat I,

WPI; 2003-625403/59.

Novel isolated polypeptide having stem cell growth factor activity, useful for promoting wound healing, and as a medicine to proliferate or support human hematopoietic stem cells or human hematopoietic progenitor

Disclosure; Pig 3; 96pp; English.

The invention relates to an isolated stem cell growth factor-like polypeptide (referred as supporting factor for proliferation of stem cells (SCR-1)) from mouse or human, or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity. Also included are an isolated polynucleotide encoding CSCR-1 (or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity, or the complement of the polymucleotide, a host cell growth factor activity, or the complement of the polymucleotide in operative association with a regulatory sequence SCR-1 polymucleotide in the host cell, that controls expression of the polymucleotide in the host cell, preparation of the SCR-1 polymucleotide (the polypeptide having an expression product of the SCR-1 polymucleotide (the polypeptide having an expression product of the SCR-1 polymucleotide (the polypeptide having an activity to support proliferation or survival of haematopoietic stem cell, with a provise that C-terminal as sequence does not comprise the as sequence appearing as ABO44439, an isolated SCR-1 polypeptide with stem cell growth factor activity and solated SCR-1 polypeptide with stem cell growth factor activity and isolated polypeptide to maintain survival of or promote proliferation of a stem cell or grown comprising the SCR-1 polypeptide or a unique segment of the SCR-1 polymucleotide or a unique segment of the SCR-1 polymucleotide or a stromal cell genetic or survived to surface, a stromal cell genetic or survived to surface, a stromal cell genetic or survived to surface, a stromal cell series or surface or surface, a stromal cell series or surface or engineered to express the SCR-1 polypeptide to support proliferation or survival of a stem cell or germ cell and an implant comprising a cell genetically engineered to express the SCR-1 polypeptide to support proliferation or survival of a stem cell or germ cell. The SCR-1 polypeptide is useful for identifying a compound that binds to the SCR-1 polypeptide and for maintaining survival of or promoting proliferation of a stem cell, a germ cell, a perm cell or a haematopoietic progenitor cell. The SCR-1 polypeptide is useful for promoting wound

WPI; 1999-024059/02.

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healing. The human haematopoletic stem cell or human haematopoletic progenitor cell culture using the SCR-1 polypeptide can replace as a graft for the conventional bone marrow transplantation or cord blood transplantation. The transplantation of haematopoletic stem cells can be employed as a therapy for treating diseases such as chronic granulomatous diseases, duplicated immunodeficiency syndrome, agammaglobulinaemia, wiskott-Aldrich syndrome, AIDS, etc., thalassaemia, haemolytic anaemia due to enzyme defect, congenital anaemia such as sicklaemia, disease etc. the SCR-1 polypeptide is useful for cell growth and morphogenesis, including tissue specific stem cell growth, epithelial cell growth and regulation, ovarian follicle development, promoting nerve cell growth, sustaining neuronal populations, cartilage remodeling, bone
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                                                                                                                                                                                                                                                                                                                                              0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone; secreted protein; protein factor; cytokine; lymphokine; interferon; colony stimulating factor; CSF; interleukin; cloning; tumour invasion; tumour suppression; immune boosting.
                                                                                                                                                                                                                       growth and immunosuppression. The present sequence is a protein homologous to Human SCR-1 protein
                                                                                                                                                                                                                                                                                                         97.8%; Score 1477; DB 6; Length 265; 100.0%; Pred. No. 3.8e-108; ive 0; Mismatches 0; Indels
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98US-00065125.
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                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                         Sequence 265 AA;
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us-09-894-912a-34.rag

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of clones ci254 (AAV83132), da2286 (AAV83133), du4105 (AAV83134), eh801 (AAV83135), ex561 (AAV83136), fimed (IAAV83139) or fr4732 (AAV83139), (all clones are deposited as ATCC 98415) and the proteins they encode are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals for example, tumour suppression/invasion activity, immune system boosting activity. The polynucleotides are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, stem cell growth factor-like protein; antiinflammatory; nootropic; neuroprotective; vulnerary; cytostatic; anticonvulsant; immunostimulant; assotropic; virucide; dermatological; tranquillilaer; cerebroprotective; osteopathic; immunodeficiency syndrome; chronic granulomatous disease; duplicated immunodeficiency syndrome; wiskott-Aldrich syndrome; AIDS; acquired immunodeficiency syndrome; agammaglobulinaemia; thalassaemia; Gaucher; disease; lysosomal storage disease; mucopolysaccharidosis; adrenal white matter degeneration; anaemia; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; thrombocytopaenia; SCID; severe combined immunodeficiency; immune disorder; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; autoimmune pulmonary inflammation; cancer; tumour; gene therapy; SCR-1; supporting factor for the proliferation of stem cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPFALERIGMKOIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNPCTKCKSGFYL 120
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                                     New polynucleotides encoding secreted human proteins - are derived from human foetal brain, adult brain, adult blood or placenta cDNA libraries, useful, e.g. as potential immunomodulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MHLRLISWLF IILNFWEYIGSQNASRGRRQRRWHPNVSQGGQGGCATCSDYNGCLSCKDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OHPSAKGNLCPPTNBTRKCTVQRKKCQKGERGKKGRERKRKKPNKGBSKBA I PDSKSLBS
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                                                                                                                                                            nucleotide sequence (NS) of the full-length protein-coding
                                                                                                                                                                                                                                                                                                                                                                                                    Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  97.8%; Score 1477; DB 2; L
100.0%; Pred. No. 4.3e-108;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                      believed to be useful for gene therapy
                                                                                                                    Claim 8; Page 63-64; 104pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE13170 standard; protein; 292 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 265; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
N-PSDB; AAV83133
                                                                                                                                                                                                                                                                                                                                                          Sequence 292 AA;
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Novel stem cell growth factor like polypeptides and polynucleotides for identifying modulators useful for treating diseases such as Alzheimer's disease, cancer, rheumatoid arthritis, osteoporosis.

Drmanac RT;

Labat I, Tillinghast JS, Sinku A, Liu C, ain B, Dickson M, Mize NK, Nishikawa M;

WPI; 2001-657166/75. N-PSDB; AAD21740.

Stache-Crain B,

rang TY,

05-APR-2000; 2000US-00543774. 28-JUN-2000; 2000US-0215733P. 09-JAN-2001; 2001US-00757552. 05-PRB-2001; 2001US-0266614P.

(KIRI ) KIRIN BEBR KK

(HYSE-) HYSEQ INC.

05-APR-2001; 2001WO-US011208

18-0CT-2001

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The patent discloses novel stem cell growth factor-like proteins and polymucleotides encoding them. Proteins of the invention are also known as supporting factor for the proliferation of stem cells (STEM—1). Stem cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell, embryonic stem cell, germ cell, germ cell, embryonic stem cell, parantopoletic progenitor cell, embryonic stem cell, parantopoletic progenitor cell, pluripotent cell or totipotent cell. The haematopoletic progenitor cell cultured using stem cell growth factor-like proteins can replace as a graft for the bone marrow transplantation or cord blood transplantation for treating a variety of diseases such as immunodeficiency syndrome, agammaglobulinaemia, wiskott-Aldrich syndrome, acquired immune deficiency syndrome (Arsonic Standard, haemolytic anaemia denote to enzyme defect, congenital anaemia degeneration, a variety of cancer and tumours. Proteins of the invention are useful for treating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, thrombocytopeania, immune deficiencies and disorders such as multiple sclerosis, systemic collupus erythematosus, thumatoid immune disorders such as multiple sclerosis, systemic lupus erythematosus, heumatoid arthritis, and autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, heumatoid arthritis, and autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, heumatoid arthritis, and autoimmune disorders such as multiple aclerosis, systemic lupus erythematosus, heumatoid arthritis, and autoimmune disorders such as such as multiple sclerosis, systemic lupus erythematosus, heumatoid arthritis, and autoimmune disorders such as an autopined inamune disorders and althritism erythematosus, heumatoid arthritism and autoimmune disorders and arthritism and autoimmune disorde
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammation. Sequences of the invention are also us.
The present sequence is human SCR-1 related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27; Page 231-232; 232pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKEI PEORENKOOOKKRKVODKOKS 265
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Best Local Similarity 100.0
Matches 265; Conservative
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WO200177169-A2

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The invention relates to human secreted or transmembrane protein (I), their fragments and is encoded by specific complementary decyribonucleic acid (cDNA) inserts (II), where the protein is substantially free from other mammalian proteins. (I) are useful for preventing, treating or meliorating a medical condition, especially immunological treatment or prevention of tumoures. (I) exhibits activity relating to angiogenesis, cytokine, cell proliferation, cell differentiation, antiinflammatory, stem cell growth factor activity and activin or inhibin-related cytokine. (I) can be used to manipulate stem cells in culture to give crise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. (I) induces the proliferation of neural cells and central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis. (I) is involved in chemotactic or chemokinetic artivity, regulation of haematopolesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopaenia
                                                                                                                                                                                                                                        Human; cytostatic; antirheumatic; antiarthritic; vulnerary; analgesic; antinflammatory; antibacterial; immunosuppressive; antiparklnsonian; meuroprotective; nootropic; osteopathic; haemostatic; vasotropic; antiulcer; fungicide; antidiabetic; antiasthmatic; antiallergic; immunostimulant; antiparasitic; secreted protein; transmembrane protein; cytokine; cell proliferation; cell differentiation; autoimmune disease; stem cell; growth factor; nervous system disease; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; osteoporosis; severe combined immunodeficiency; SCID; infection; multiple sclerosis; rheumatoid arthritis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel secreted or transmembrane protein and polymucleotide encoding the protein, useful for diagnosis and treatment of neurological disorders, cancer, autoimmune diseases, bone disorders and lung or liver fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collins-Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 207; Page 203-204; 284pp; English.
SKEI PEQRENKQQQKKRKVQDKQKS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lavallie ER,
Spaulding V;
                                                                                        ABP61846 standard; protein; 292 AA
                                                                                                                                                                                                        Human polypeptide SEQ ID NO 200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-DEC-2000; 2000US-00745763.
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                                                                                                                                                                   04-OCT-2002 (first entry)
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N-PSDB; ABQ92060.
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MERBERG D.
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LAVALLIB B
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(SPAU/)
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                                                     RESULT 14
                                                                        ABP61846
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Evans C;

and for regeneration of bone, cartilage, tendon, ligament and/or nervetissue growth and in tissue repair, healing of burns, incisions, ulcers, for treating osteoprosis, osteoarthritis, bone degenerative disorders or periodontal disease. (1) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. (II) is useful to express recombinant protein, as markers for tissues in which the corresponding protein is preferentially expressed and in gene therapy. The present sequence is that of a polypeptide of the invention ö 240 120 120 180 180 240 9 1 MHIRLISWIFIILNFWRYIGSQNASRGRRORRMHPNVSQGCQGGCATCSDYNGCLSCKPR LPPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYL 61 LFPALERIGMKOIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNPCTKCKSGFYL HIGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII 121 HIGKCIDNCPEGIEANNHTWECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII 181 OHPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGBSKEAIPDSKSLBS 1 MHIRLISWLFIILNFWRYIGSONASRGRRORRMHPNVSOGCOGGCATCSDYNGCLSCKPR Gaps Human; secreted; stem cell growth factor; cytostatic; haemostatic; neuroprotective; immunostimulant; leukaemia; haemophilia; cancer; degenerative disease; Alzhelmer's disease; food supplement; ; 0 Length 292; 97.8%; Score 1477; DB 5; Length 2 100.0%; Pred. No. 4.3e-108; ive 0; Mismatches 0; Indels Human secreted protein clone da_288_6 #25. 241 SKEIPEQRENKQQQKKRKVQDKQKS 265 241 SKEIPEQRENKQQQKKRKVQDKQKS 265 ABR62114 standard; protein; 292 AA 30-AUG-2001; 2001US-0316368P. 10-DEC-2001; 2001US-0339739P. 19-APR-2002; 2002US-00125852. 30-AUG-2002; 2002WO-US027746. (first entry) 265; Conservative immunological disorder Similarity (HYSE-) HYSEQ INC Sequence 292 AA; WO2003029405-A2 Homo sapiens. 18-AUG-2003 .0-APR-2003. 121 Query Match Best Local S ABR62114; rang YT; RESULT 15 ABR62114 Matches 8888888888888888888 ð 셤 ŝ 셤 셤 셤 Š ð ð

WPI; 2003-381616/36.

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New stem cell growth factor-like polypeptides and polymucleotides, useful for treating e.g. leukemia, hemophilia and degenerative diseases like Alzheimer's disease, and for inducing immune response.
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Disclosure; Fig 2; 151pp; English.

The invention relates to new stem cell growth factor-like polypeptides and polynucleotides. The stem cell growth factor-like polypeptides and polynucleotides are useful for inducind differentiation of embryonic and adult stem cells to give rise to different cell types, for treating e.g. leukaemia, haemophilia and degenerating different cell types, for treating e.g. leukaemia, haemophilia and degenerating use tissues and organs that considered in need of transplanted tissues. The polynucleotides are useful as hybridisation probes, oligomers or primers for PCR, for chromosome and gene mapping, in recombinantly producing protein, in concerning antisense DNA or RNA, in diagnostics as expressed sequence tags for identifying expressed genes, and for inducing immune response. The polypeptides are useful for generating antibodies that specifically bind the polypeptides are useful for generating antibodies that specifically chind the polypeptides as molecular weight markers, and as a food supplement (e.g. protein or amino acid supplement, and as a carbon, nitrogen or carbohydrate source). Compositions comprising the polypeptides or polymucleotides are useful for the diagnosis, treatment or prevention of cancers, and other immunological disorders. The current sequence represents a human secreted protein clone da_288_6 

Sequence 292 AA;

LFPALERIGHMOLGVCLSSCPSGYYGTRYPDINKCTXCKADCDTCFNKNFCTKCKSGFYL 120 HLGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGPKRGTETRVREII 180 121 HIGKCLDNCPEGLEANNHTWECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII 180 QHPSAKGNI,CPPTNBTRKCTVQRKKCQKGERGKKGRERKRKKDNKGESKEAI PDSKSLES 240 LFFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYL 120 QHPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGESKBAIPDSKSLES 240 1 MHLALISWLFIILAFWEYIGSQNASRGRRQRRWHPNVSQGCQGGCATCSDYNGCLSCKPR 60 1 MHLRLISWLFIILNFWBYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR Gaps ö Length 292; 0; Indels 97.8%; Score 1477; DB 6; Li 100.0%; Pred. No. 4.3e-108; vative 0; Mismatches 0; 241 SKRIPEQRENKQQOKKRKVQDKQKS 265 SKEIPEORENKOOOKKRKVODKOKS 265 Query Match 97.8 Best Local Similarity 100. Matches 265; Conservative 61 19 121 181 181 셤 ò g 쉱 8 g 셤 ઠે 8 ò

rch completed: June 29, 2004, 16:59:53 time : 50.5178 secs Search Job tim 2, Appli 3, Appli 10, Appl 10, Appl 10, Appl 10, Appl 103, Appli 4, Appli 2, Appli

Appli Appli Appl

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737 YPGDTAARKCRR-----HHQEMNT 779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08284941
; Sequence 2, Application US/08284941
; Patent No. 5863766
; Patent No. 5863766
; Patent No. 5863766
; Patent No. 5863768
; APPLICANT: BARR, PHILIP J
; APPLICANT: KIERER, MCCHABL C
; TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSES: ADDRESSE:
; ADDRESSES: ADDRESSE:
; CITY: PALO ALTO SQUARE
; CITY: PALO ALTO
; STREET: CALIFORNIA
; COUNTRY: USA
; CITY: 9106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,941
FILING DATE: 2 August 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NEELEY PH.D., RICHARD L.
REGISTRATION NUMBER: 30092
REFERENCE/DOCKET NUMBER: 30092
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERAX: 308016 COOLEY PA
INFORMATION POR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
TENANTH: 969 amino acids
US-09-640-173-186
US-09-713-550-186
US-09-113-550-186
US-09-113-825-2
US-08-185-432-17
US-08-185-432-17
US-08-185-432-17
US-08-185-432-17
US-08-132-769-5
PCT-US93-03164-10
US-08-857-076-103
US-08-857-076-103
US-08-857-076-103
US-08-858-864-6418-18
US-08-249-687C-2
US-08-655-819-2
US-08-655-819-2
US-08-655-819-2
US-08-854-6418-18
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TYPE: amino acid
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Best Local Similarity 28.8'
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MOLECULE TYPE: protein
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Sequence 2, A
Sequence 23,
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1510
1 MHLRLISWLPIILNPMBYIG......QQKKRKVQDKQKSVSVSTVH 272
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Sequence 21,
Sequence 21,
Sequence 18,
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Sequence 7
Sequence 1
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Sequence
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6: /cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-447-642-7
US-09-245-503-2
PCT-US93-02147A-2
US-08-525-940-21
US-08-976-838-23
US-08-976-838-18
US-08-976-838-18
US-08-92-14-555B-2
US-09-214-555B-2
US-09-214-555B-2
US-09-214-555B-2
US-09-214-555B-2
US-09-905-125A-4
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US-09-132-769-1
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                                                                                                                                                                                                                                                                                                                                                            389414 seqs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                     - protein search, using sw model
                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                                                                                                    Title:
Perfect score:
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7;

Gaps

39;

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PCT-US93-02147A-2
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                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2
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CLSSCPSGYYGTRYPDINKCTKCKADCDTCPNK-NFCTKCKSGPYLHLGKCLDNCPEGLR 134
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                                                                                                                                                                                                                                 Sequence 2, Application US/08447642
Patent No. 5989800
GENERAL INFORMATION:
APPLICANT: BARN, PHILIP J
APPLICANT: RIBFER, MICHAEL C
TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
CORRESPONDENCE COOLEY GOUWARD CASTRO HUDDLESON & TATUM
STREET: FIVE PALO ALTO SQUARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 969;
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nes 54; Indels
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ZIP: 94306

ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,642
FLING DATE: 23-MAY-1995
CLASSIFICATION NUMBER: US 08/284,941
PRICK APPLICATION NUMBER: US 08/284,941
PLING DATE: 2 August 1994
ATYONRY/AGENT INFORMATION:
NAME: REGILEY PH.D., RICHARD L.
REGISTRATION NUMBER: 30092
                                                                                     135 ANNHIMECVSIVHCEVSEWNPWSPCTKKGKTCG 167
                                                                                                                                ---TCG 853
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28.8%; Pred. No. 1.36
tive 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: CHIR-009/01US TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 843-5070
TELEFAX: (415) 857-0663
TELEX: 380816 COOLEY PA
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
IENGTH: 969 amino acids
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
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Best Local Similarity
Matches 44; Conserv
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RESULT 3 US-09-236-503-2

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                                                                                                                                                                                                                                                                                                                                                              13.7 NHTMB-----NPWSPCTKK 162
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                                                                                                                                                                             20 GSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNG--CLSCKPRLFFALERIGMKQIGVCL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
                                                                                        10.7%; Score 162; DB 2; Length 799; 22.3%; Pred. No. 9.8e-06; Live 33; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 799;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: PLOSPDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/976,838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.7%; Score 162; DB 2;
22.3%; Pred. No. 9.8e-06;
tive 33; Mismatches 81.
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STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23, Application US/08976838
Patent No. 5981259
                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 GKTC-----GPKRGTE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INPORMATION:
NAME: Connell, Gary J.
REGISTATION NUMBER: 2848
REPERENCE/DOCKET NUMBER: 2848
TELECOMMUNICATION INFORMATION:
TELEFRAK: (303) 863-9700
TELEFRAK: (303) 863-9700
INPORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                        Query Match
Best Local Similarity 22.3*
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 799 amino acids
amino acid
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TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-976-838-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
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Best Local Similarity
Matches 55; Conserva
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STATE: Colorado
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                                                US-08-525-940-23
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                                                                                                                                                                                                                                                                                                                                                           18 YIGSQNASRGRRQRRMHPNVSQGCQGCATCSD--YNGCLSCKPRLFFALERIGMKQIGV
                                                                                                                                                                                                                                                                                                                  39;
                                                                                                                                                                                                                                                                        DB 5; Length 969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Franzusoff, Alex
APPLICANT: Miranda, Luis R.
APPLICANT: Miranda, Luis R.
APPLICANT: Wolf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
TITLE OF INVENTION: ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                      Query Match 11.5%; Score 173.5; DB 5; Length Best Local Similarity 28.8%; Pred. No. 1.3e-06; Matches 44; Conservative 16; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 ANNHIMECVSIVHCEVSEWNPWSPCTKKGKTCG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 01-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION WINGER: US 08/088,322
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTATION NUMBER: 2848-11-C1
REFERENCE/DOCKET NUMBER: 2848-11-C1
TELEPHONE: (303) 863-920
TELEPHONE: (303) 863-923
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2848-11-C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23, Application US/08525940 Patent No. 5866351
                    TELEPHONE: (415) 494-7622
TELEFAX: (415) 857-0663
TELEX: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 969 amino acide
TYPE: amino acide
TYPE: 1nnear
    TELECOMMUNICATION INFORMATION
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LENGTH: 799 amino acids
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STATE: Colora
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137 NHTME-----NPWSPCTKK 162
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                                                                                                                                                                                                                                            ---TRVRBIIQHPSAKGNLCPPTNETRKCTV 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 GSQNASRGRRORRMHPNVSQGCQGCATCSDYNG--CLSCKPRLPFALERIGMKQIGVCL
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                                                                                 78 SSCPSG-YYGTRYPDINKCTKCKADCDTCFNKNPCTKCKSGFYLHLGKCLDNCPEGLBAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.7%; Score 162; DB 2; Length 881; 22.3%; Pred. No. 1.1e-05; trive 33; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C2
TELECOMMUNICATION INFORMATION:
TELEPRIONE: (303) 863-9700
TELEPRIONE: (303) 863-9700
TELEFRA: (303) 863-023
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                 163 GKTC-----GPKRGTB------
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; Sequence 21, Application US/08976838
; Patent No. 5981259
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
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Best Local Similarity
Matches 55; Conserva
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Denver
STATE: Colora
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                             78 SSCPSG-YYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLHLGKCLDNCPEGLEAN 136
                                                                                                          13.7 NHTME-----NPWSPCTKK 162
                                                                                                                                                                                                                                                 ---TRVREIIQHPSAKGNLCPPTNBTRKCTV 201
                                                                                                                                                                                                                                                                                      725 DISCLICNGPGFKNCTSCPSGYLLDLGMCQMGAICKDATBESWAEGGFCMLVKKNNLC-- 782
      GSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNG--CLSCKPRLFFALERICWKQIGVCL 77
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APPLICANT: Miranda, Luis R.
APPLICANT: Miranda, Luis R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES
TITLE OF INVENTION: ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McInton
STREET: 1700 Lincoloria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNDERR: US 08/368,852
PILING DATE: 01-JAN-1995
PRIOR APPLICATION NUMBER: US 08/088,322
PILING DATE: 07-JUL-1993
APPLICATION NUMBER: US 08/088,322
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                 163 GKTC-----GPKRGTB------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21, Application US/08525940 Patent No. 5866351 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     881 amino acids
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Best Local Similarity 22.3
Matches 55; Conservative
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US-08-525-940-21
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781 GQDCQPCHRFCATCAGAGGADGCINCTBGYFMBDGRCVQSCSISYYPDHSSRNGYKSCRKC 840
                                                                                                                                                                     --IVHCEVSEW-----NPWSPCTKK 162
                                                                                                                            ---TRVREIIQHPSAKGNICPPTNBTRKCTV 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 781 GODCOPCHRPCATCAGAGADGCINCTEGYFMEDGRCVQSCSISYYPDHSSENGYKSCKKC 840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              841 DISCLICKGEGERKKTSCPSGYLLDLGMCQMGAICKDATEBSWABGGECMLVKKNNLC-- 898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18, Application US/08976838
Patent No. 5981259
GENERAL INFORMATION:
TAPLICANT: Franzusoff, Alex
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROFEASE NUCLEIC ACID
NUMBER OF INVENTION: MILECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 915;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CAURENY APPLICATION DATA:
APPLICATION NUMBER: US/08/976,838
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.7%; Score 162; DB 2;
22.3%; Pred. No. 1.1e-05;
tive 33; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION UNDRER: 32,020
REFERENCE/DOCKET UNDRER: 2848-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEPAK: (303) 863-9700
TELEPAK: (303) 863-0223
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                               163 GKTC-----GPKRGTB-----
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amino acid
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MOLECULE TYPE: protein
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STATE: Colorado
COUNTRY: U.S.A.
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137 NHTMB---
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                                                                                                                                                                         807 DISCLTCNGPGFKNCTSCPSGYLLDLGMCQMGAICKDATBESWAEGGFCMLVKNNLC-- 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSCPSG-YYGTRYPDINKCTKCKADCDTCPNKNPCTKCKSGPYLHLGKCLDNCPEGLEAN 136
13.7 NHTME-----NPWSPCTKK 162
                                                                                                                                   -----TRVREIIQHPSAKGNLCPPTNBTRKCTV 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Franzusoff, Alex
APPLICANT: Miranda, Luis R.
APPLICANT: Miranda, Luis R.
APPLICANT: Wolf Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
TITLE OF INVENTION: ENCODING SAID PROTEASES
OWNERS OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1700 Lincoln Street, Suite 3500
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,852
FILING DATE: 01-JAN-1995
PRIOR APPLICATION NUMBER: US 08/088,322
PILING DATE: 07-JUL-1993
ATTORNEY JAENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 2848-11-C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                            163 GKTC-----GFKRGTB-----
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Patent No. 5866351
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 915 amino acids
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amino acid
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                                                                                                                                                                                                                                                               202 QRKKCQK 208
                                                                                                                                                                                                                                                                                                                             865 QRKVLQQ 871
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ses 55; Conserv
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US-08-525-940-18
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SEQUENCE CHARACTERISTICS
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GENERAL INFORMATION:

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APPLICANT: INFORMATION:

APPLICANT: INFORMATION:

TITLE REFERENCE: PRO-PROTEIN CONVERTING ENZYME

TITLE REFERENCE: PRO-PROTEIN CONVERTING ENZYME

CURRENT REPLICANTON NUMBER: US/09/214,555B

CURRENT FILING DATE: 1999-01-04

PRIOR APPLICATION NUMBER: 00/021,008

FRIOR APPLICATION NUMBER: 2,203,745

PRIOR FILING DATE: 1997-04-25

NUMBER OF SEQ ID NOS: 9

SEQ ID NO 2

LENGTH: 915
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Patent No. 6380171
GENERAL INFORMATION BE RECHERCHE CLINIQUE DE MONTRAL
TITLE OF INVENTION PRO-PROTEIN CONVER ENZ
TITLE OF INVENTION PRO-PROTEIN CONVER ENZ
CURRENT APPLICATION UNMERS: 1999-01-04
FRIOR PELICATION NUMBER: 60/021,008
FRIOR PELICATION NUMBER: 2,203,745
PRIOR PLINIG DATE: 1996-07-26
PRIOR PLINIG DATE: 1996-07-26
PRIOR PLINIG DATE: 1996-07-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
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TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
202 QRKKCQK 208
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US-09-214-555B-7
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                                                          78; Gaps
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                                                                                                                 20 GSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNG--CLSCKPRLFFALERIGMKQIGVCL
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10.7%; Score 161; DB 1; Length 288;
Best Local Similarity 28.2%; Pred. No. 3.8e-06;
Matches 46; Conservative 25; Mismatches 52; Indels
Query Match 10.7%; Score 162; DB 4; Length 915; Best Local Similarity 22.3%; Pred. No. 1.1e-05; Matches 55; Conservative 33; Mismatches 81; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
APPLICANT: Franzusoff, Lis R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
TITLE OF INVENTION: RNCODING SAID PROTEASES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COPERATING SYSTEM: FC-COMPSIDES
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/368,852
FILING DATE: 05-JAN-1995
CLASSIFICATION: 435
ATTONEX/AGBNT INPORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 37,459
TELEPHONE: 303/863-9700
TELEPHONE: 303/863-9700
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STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
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; Sequence 15, Application US/08368852
; Patent No. 5691183
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INFORMATION FOR SEQ ID NO: 15:
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amino acid
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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Grimaldi, Christopher J.
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Patent No. 6664376
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenati, Avi
APPLICANT: Botstein, David
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary E.
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 24.94
Matches 60; Conservative
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Sao, Wei-Qiang
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Baton, Dan L.
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                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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                                           93 NKCTKCKADCDTCPNK--NPCTKCKSGPYLH--LGKCLDNCPEGLEANNHTMECVSIVHC 148
                                                                                 -- 112
    PECSEVGCDGPGPDHCND---CL---HYYYKLK----NNTRICVSSCPPGHY---HADK 58
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APPLICANT: Wood, William, I.
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITILE OF INVENTION: Acids Encoding the Same
                                                                   149 EVSEWNPWSPCTKKGKTC-GPKRGTETRVREIIOHPSAKGNLC 190
                                                                                                                                                           113 -----BRCSENXKTCTEPHXCTECR-----DGLSLQGSRC 142
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CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
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PFILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
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PILING DATE: 1999-11-29
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APPLICATION NUMBER: PCT/US99/30095
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APPLICATION NUMBER: PCT/US99/20944
FILING DATE: 1999-09-13
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IOR APPLICATION NUMBER: US 60/146,222
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Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
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Paoni, Nicholas F.
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Gerritsen, Mary E.
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Mather, Jennie P.
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Ashkenazi, Avi
Botstein, David
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Baton, Dan L.
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Sao, Wei-Qiang
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                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                               272 -----QCEISKCP--QPCRNGGKCIG---KSKCKCSKGYQGDLCSKPVCEPGCGAHG 318
                                                                                                                ----LSCKPRLPPALERIGMKQIGVCLSS----C 80
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CANT: Wood, William, I.
OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
OF INVENTION: Acids Encoding the Same
                                                        83; Gaps
  Length 379;
                                                        72; Indels
10.5%; Score 158.5; DB 4; 24.9%; Pred. No. 8.5e-06; tive 26; Mismatches 72;
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PRIOR APPLICATION NUMBER: PCT/USOU/04414
PRIOR APPLICATION NUMBER: PCT/USOU/04414
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
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ORGANISM: Homo sapiens
CURRENT FILING DATE:
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81 PSGYYGTRYPDINKCTKC-KADCD-TCPNKNFCTKCKSGFYLHIGKCLDNCPEGLEANNH 138 182 CPGGCRNGGFCNERRICECPDGFHGPHCRKALKTPRCMNG-----GLKVTPGFCIC 232 233 PPGPYG------VNCDKANCSTTCFNGGTC-----FY--PGKCI--CPPGLEGE-- 271 139 TMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQHPSAKGNLCPP---- 192 41 CQGCCAT---CSDYNGC----C 80 Query Match 10.5%; Score 158.5; DB 4; Length 379; Best Local Similarity 24.9%; Pred. No. 8.5e-06; Matches 60; Conservative 26; Mismatches 72; Indels 83; Gaps 요 Š 음 중 음

272 ------QCEISKCP--QPCRNGGKCIG---KSKCKCSKGYQGDLCSKPVCEPGCGAHG 318 193 -TNETRKCTVQRKKKCOKGERGKKGRERKRK-----KPNKGESKEAIPDSKSLESSKRIP 245 :| || :| | :| | ::| | 319 TCHEPNKC-----QCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKASEERBDPP 373

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246 B 246

374 B 374

Search completed: June 29, 2004, 17:04:02 Job time : 15.1942 secs

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Sequence 10, Appl
Sequence 34, Appl
Sequence 13, Appl
Sequence 16, Appl
Sequence 166, Appl
Sequence 48, Appl
Sequence 25, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 172, Appl
Sequence 172, Appl
Sequence 172, Appl
Sequence 176, Appl
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1 MHLRLISWLFIIIANFMEYIG......QQKKRKVQDKQKSVSVSTVH 272
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Copyright (c) 1993 - 2004 Compugen Ltd.
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-192-1779 -912A-14 -912A-14 -912A-14 -952-21 -952-21 -952-21 -042-13 -042-13 -042-13 -042-13 -952-3 -952-3 -952-3 -952-3 -952-3 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-13 -952-1	3.2e
16 981 65.0 180 12 US-10-087-192-1779 17 903 59.8 160 10 US-99-94-912A-14 18 656 43.4 263 14 US-10-276-774-174 20 648.5 42.9 243 14 US-10-276-774-174 21 638 42.9 243 14 US-10-125-652-21 22 638 42.9 243 14 US-10-125-652-21 23 582.5 38.6 243 14 US-10-125-652-13 24 589.5 39.0 243 14 US-10-125-652-13 25 582.5 38.6 243 14 US-10-125-652-13 25 582.5 38.6 243 14 US-10-125-652-13 26 53.1 32.2 14 US-10-125-652-13 27 578 38.3 23.1 122.1 4 US-10-125-652-13 28 540.5 35.8 229 14 US-10-125-652-13 29 540.5 35.8 229 14 US-10-125-652-13 20 402.5 26.7 190 12 US-10-67-192-873 31 239.5 11.3 4.1 10 US-09-894-912A-20 32 540.5 35.8 229 14 US-10-125-652-13 32 23.1 14.6 42 10 US-09-894-912A-20 34 186.5 12.4 16 10 US-09-894-912A-20 35 177.5 11.5 569 10 US-09-894-912A-20 36 177.5 11.5 569 10 US-09-894-912A-20 37 186.5 10.6 337 12 US-10-135-820-64 3 160.5 10.6 343 12 US-10-135-820-64 41 160.5 10.6 343 12 US-10-357-820-64 42 160.5 10.6 343 12 US-10-357-820-64 43 160.5 10.6 343 12 US-10-357-820-64 44 160.5 10.6 343 12 US-10-357-820-64 45 160.5 10.6 343 12 US-10-357-820-64 46 160.5 10.6 343 12 US-10-357-820-64 47 160.5 10.6 343 12 US-10-357-820-64 48 160.5 10.6 343 12 US-10-357-820-64 49 160.5 10.6 343 12 US-10-357-820-64 40 160.5 10.6 343 12 US-10-357-820-64 41 160.5 10.6 343 12 US-10-357-820-64 42 160.5 10.6 343 12 US-10-357-820-64 43 160.5 10.6 343 12 US-10-357-820-64 44 160.5 10.6 343 12 US-10-357-820-64 45 160.5 10.6 343 12 US-10-357-820-64 45 160.5 10.6 343 12 US-10-357-820-64 46 160.5 10.6 343 12 US-10-357-820-64 47 160.5 10.6 343 12 US-10-357-820-64 48 160.5 10.6 343 12 US-10-357-820-64 49 180.5 10.0 3000044792A1 ENERRAL INVERTION NUMBER: 06/215,733 PRICE PLING DATE: 2001-00-05 PRICE PLING DATE: 2001-00-05 PRICE PLING DATE: 2000-06-28 PRICE PLING DATE: 2000-06-38 PRICE PLING DATE: 2000-06-38 PRICE PLING DAT	Score Pred.
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16 991 65.0 180 12 US-10 18 903 59.8 160 10 US-09 19 656 42.9 160 12 US-10 20 648.5 42.9 243 14 US-10 21 644 42.6 265 14 US-10 22 626.5 41.5 236 15 US-10 24 589.5 39.0 243 14 US-10 25 582.5 38.6 243 16 US-10 26 582.5 38.6 243 16 US-10 27 578 38.3 250 14 US-10 29 540.5 38.8 229 14 US-10 30 402.5 26.7 190 12 US-10 31 365.5 26.7 190 12 US-10 32 23.5 15.9 131 14 US-10 33 239.5 15.9 131 14 US-10 34 221 14.1 37 10 US-09 35 202 11.8 43 14 US-10 36 202 11.8 43 14 US-10 37 186.5 10.6 343 12 US-10 40 160.5 10.6 343 12 US-10 40 160.5 10.6 343 12 US-10 41 160.5 10.6 343 12 US-10 42 160.5 10.6 343 12 US-10 43 177.5 11.8 PAPLICATION NUMBER: US/09/89 CURRENT PILING DATE: 2001-04-05 PRIOR APPLICATION NUMBER: CO/26,614 PRIOR PILING DATE: 2000-06-28 PRIOR APPLICATION NUMBER: CO/26,614 PRIOR PILING DATE: 2000-06-28 PRIOR PILING DATE: 2000-04-05 PRIOR PILING DATE: 2	atch
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SOFTWARE: Patentin version 3.0
SEQ ID NO 34
LENGTH: 272
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; ORGANISM: Homo sapiens
US-09-894-912A-34
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RESULT 3 US-10-125-852-23 ; Sequence 23, Application US/10125852

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Publication No. US20030032034A1
GENERAL INFORMATION:
APPLICATION:
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH PACTOR-:
TITLE OF INVENTION: METHODS AND POLYNUCLEOTIDES
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REPERENCE: HYS-43A
CURRENT APPLICATION NUMBER: US/10/125,852
CURRENT FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: US 60/316,368
PRIOR APPLICATION NUMBER: US 69/799,451
PRIOR APPLICATION NUMBER: US 69/799,451
PRIOR PILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
SEQ ID NO 23
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US-09-894-912A-13

US-09-894-912A-13

US-09-894-912A-13

Sequence 13, Application US/09044792A1

Sequence 13. Application No.

US20030044792A1

SEQUENCE 1 INFORMATION:

APPLICANT: Tang et al.

APPLICANT: Tang et al.

APPLICANT: Tang et al.

TITLE OF INVENTION: FACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: FACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES

CURRENT APPLICANTON NUMBER: US/09/894,912A

CURRENT APPLICANTON NUMBER: US/026,614

PRIOR PILING DATE: 2001-04-05

PRIOR PILING DATE: 2000-06-28

PRIOR PILING DATE: 2000-06-28

PRIOR PILING DATE: 2000-06-05

PRIOR PILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 48

SOFTWARRE PATENTIN VERSION 3.0

SEQ ID NO 13

TYPE: PRT

CORGANISM: Homo sapiens
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Best Local Similarity 100.0%; Pred. No. 5.2e-115;
Matches 272; Conservative 0; Mismatches 0; 1
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US-10-125-852-23
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61 LPPALERIGAKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNRNPCTKCKSGPYL 120
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181 OHPSAKGNLCPPTNBTRKCTVORKKCOKGERGKKGRERKRKRPNKGESKRAIPDSKSLES 240
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                                                                                                                                                                                                                                                                                                                                                                                                                       Merberg, David
Treacy, Maurice
Spaulding, Vikh
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/745,763
FILING DATE: 18-Jun-2000
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100.0%; Pred. No. 2.7e-112;
tive 0; Mismatches 0;
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ADDRESSER: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 166:
US-09-745-763-166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: CUMCHOWN ATTORNEY AGENT INFORMATION:
NAME: SPICHOGE, SUZZING A. REGISTRATION NUMBER: 41, 323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 496-8284
TELEPRAX: (617) 496-8284
TELEPRAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 166:
                                                                                               241 SKEIPEORENKOOOKKRKVODKOKS 265
                                                                                                                                                                                                                                                                                                                       McCoy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa A.
Evans, Cheryl
                                                                                                                                                                                                                     Sequence 166, Application US/09745763
Patent No. US20020065394A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
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STRANDEDNESS: «Unknown»
TOPOLOGY: linear
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COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 265; Conservative
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Publication No. US20030044792A1

GENERAL INFORMATION:
APPLICANT: Tang et al.
TITLE OF INVENTION: PACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES
FILER REPERENCE: 28110/3726A

CURRENT APPLICATION NUMBER: US/09/894,912A

CURRENT PILING DATE: 2002-05-10

PRIOR APPLICATION NUMBER: 60/266,614

PRIOR PILING DATE: 2001-04-05

PRIOR PILING DATE: 2001-03-05

PRIOR PILING DATE: 2001-03-05

PRIOR PILING DATE: 2001-04-05

PRIOR PILING DATE: 2001-04-05

PRIOR PILING DATE: 2000-06-28

PRIOR PILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PatentIn version 3.0

SEQ ID NO 26
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Pred. No. 2.5e-112;
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                         Query Match 99.7%; Score 1505; DE
Best Local Similarity 100.0%; Pred. No. 1.34
Matches 271; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 2.5
Matches 265; Conservative 0; Mismatches
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US-09-894-912A-26
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US-09-894-912A-26
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FULLICATION NO. 02-02-03-04-19-24-11

GENERAL INFORMATION:

APPLICAMY: Tang et al.

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH

TITLE OF INVENTION: METHODS AND POLYNUCLEOTIDES

PILE REFERENCE: 28110/37560A

CURRENT APPLICATION NUMBER: US/09/894,912A

CURRENT APPLICATION NUMBER: US/09/894,912A

PRIOR PILING DATE: 2001-04-05

PRIOR PILING DATE: 2001-04-05

PRIOR FILING DATE: 2001-06-26

PRIOR PILING DATE: 2001-06-26

PRIOR PILING DATE: 2001-01-09

SEQ ID NOS: 48

SOFTWARE: PATCHTIN VERSION 3.0

SEQ ID NOS: 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                  Query Match
97.8%; Score 1477; DB 14;
Best Local Similarity 100.0%; Pred. No. 2.7e-112;
Matches 265; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 92.7%; Score 1400; DB 10; Best Local Similarity 100.0%; Pred. No. 4.3e-106; Matches 251; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 SKEIPEQRENKQQXKRKVQDKQKS 265
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PRIOR FILING DATE: 2001-08-30
PRIOR PELICATION NUMBER: US 09/799,451
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
SEQ ID NO 25
LENGTH: 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-894-912A-16; Sequence 16, Application US/09894912A; Publication No. US20030044792A1
                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
US-10-125-852-25
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ORGANISM: Homo sapiens
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Publication No. US20030032034A1
GENERAL INFORMATION:
FILLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH FACTOR-I
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: HYS-43A
FURRENT APPLICATION NUMBER: US/10/125,852
CURRENT PILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: US 60/316,368
                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH
TITLE OF INVENTION: PACTOR-LIKE POLYPEPTIDES AND POLYNUCLECTIDES
TITLE OF INVENTION: PACTOR-LIKE POLYPEPTIDES AND POLYNUCLECTIDES
TILLE OF INVENTION: PACTOR-LIKE POLYPEPTIDES AND POLYNUCLECTIDES
CURRENT FILING DATE: 2012-05-10
PRIOR PILING DATE: 2001-05-10
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-06-28
PRIOR PILING DATE: 2001-06-28
PRIOR PILING DATE: 2001-06-28
PRIOR PILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR PRIOR FILING DATE: 2001-01-09
PRIOR PRIOR FILING DATE: 2001-01-09
PRIOR PRIOR FILING DATE: 2001-01-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 HLGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII 180
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      181 QHPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGESKEA1PDSKSLES 240
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                                                               241 SKEIPEQRENKQQQKKRKVQDKQKS 265
                                                                                                241 SKEIPEQRENKQQQKKRKVQDKQKS 265
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                                                                                                                                                                                                                                                      Sequence 48, Application US/09894912A Publication No. US20030044792A1 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 265; Conservative
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US-09-894-912A-48
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US-10-125-852-25
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LENGTH: 292
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GENERAL INFORMATION:
APPLICANT: CECCARDI, Toni et al.
TITLE OF INVENTION: ISSLATED HUMAN SECRETED PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: CLO001247
CURRENT APPLICATION NUMBER: US/10/185,770
PRIOR PILING DATE: 2002-07-01
PRIOR PILING DATE: 2001-07-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PASLERQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 HIGKCLDNCPEGLEANNHIWECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MHIRLISWLFIILNFWEYIGSQWASRGRRQRRWHPNVSQGCQGGCATCSDYNGCLSCKPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 225;
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Fublication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Morris, David W.
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT PELIORION NUMBER: US/10/087,192
CURRENT PELIOR DATE: 2002-03-01
PRIOR PELICATION NUMBER: US 09/747,377
PRIOR PLING DATE: 2000-12-22
PRIOR PILING DATE: 2001-03-01
PRIOR PILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOUTHARE: FREEER FACTOR WINDER: US 09/798,586
SEQ ID NO 1782
SEQ ID NO 1782
LUNG DATE: 2001-03-02
SEQ ID NO 1782
LUNG THE SECTION NUMBER: US 09/798,586
SEQ ID NO 1782
SEQ ID NOS: 2059
SEQ ID NOS: 2059
SEQ ID NOS: 2059
SEQ ID NOS: 2059
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100.0%; Pred. No. 2.2e-96;
tive 0; Mismatches 0;
Sequence 4, Application US/10185770 Publication No. US20030022217A1
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Best Local Similarity 100.
Matches 225; Conservative
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CORGANISM: Homo sapiens
US-10-185-770-4
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US-10-087-192-1782
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US-10-087-192-1782
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TITLE OF INVENTION: PACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: PACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES
TILLE OF ILLUS DATE: 2010/37260A
CURRENT PILING DATE: 2002-05-10
FRIOR PRILING DATE: 2001-04-05
FRIOR PILING DATE: 2001-04-05
FRIOR APPLICATION NUMBER: 60/266,614
FRIOR PILING DATE: 2001-02-05
FRIOR PILING DATE: 2001-02-05
FRIOR PILING DATE: 2001-02-05
FRIOR FILING DATE: 2001-03-05
FRIOR FILING DATE: 2001-01-09
FRIOR FILING DATE: 2001-04-05
FRIOR FILING DATE: 2000-04-05
FRIOR PILING DATE: 2000-04-05
                                      61 SGYYGTRYPDINKCTKCXADCDTCPNKNFCTKCKSGFYLHLGKCLDNCPEGLEANNHTME 120
                                                                                                                                                                          121 HLGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII 180
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SGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLHLGKCLDNCPEGLEANNHTME 141
                                                                                                                                   CVSIVHCEVSEWNPWSPCTKKGKTCGPKRGTETRVREIIQHPSAKGNLCPPTNETRKCTV 201
                                                                                                                                                                                                                                                                         ORIKKCOKGERGKKGRERKRKKPNKGESKBAIPDSKSLESSKEIPBORENKOQOKKRKVOD 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LPFVLERIGAKQIGVCLSSCPSGYYGTRYPDINKCTKCKVDCDTCFNKNPCTKCKSGFYL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 32, Application US/09894912A; Publication No. US20030044792A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             262 KQKSVSVSTVH 272
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ORGANISM: Mus musculus
US-09-894-912A-32
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US-10-185-770-4
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APPLICANT: Zhong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOL
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                                                                                                                                                                                                                                                            1 MHIRLISWLPIILNFWBYIGSONASRGRRORRWHPNVSQGCQGGCATCSDYNGCLSCKPR
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                   4.
                                                                                                                                                                       Query Match 78.3%; Score 1183; DB 15; Length 239; Best Local Similarity 97.7%; Pred. No. 1.9e-88; Matches 211; Conservative 0; Mismatches 1; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 REIIQHPSAKGNLCPPTNETRKCTVQRKKCQKGERG 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 21402-290 B
CURRENT APPLICATION NUMBER: US/10/094,886
CURRENT FILING DATE: 2002-03-07
PRIOR PELING DATE: 2001-03-08
PRIOR PELING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/313,182
PRIOR PELING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/288,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 176, Application US/10094886 Publication No. US20040002120A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Taupier, Raymond J., Jr.
Miller, Charles
Casman, Stacie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shenoy, Suresh
Padigaru, Muralidhara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shimkets, Richard
Rastelli, Luca
Spaderna, Steven
LaRochelle, William
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kekuda, Ramesh
APPLICANT: Tchernev, Velizar T.
APPLICANT: Liu, Xiaohong
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Boldog, Ferenc
Guo, Xiaojia
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Gerlach, Valerie
Pochart, Pascal
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Gangolli, Bsha
Gusev, Vladimir
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NUMBER OF SEQ ID NOS: 298
SOFTWARE: Patentin 2.1
SEQ ID NO 172
LENGTH: 239
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Gorman, Linda
                                                                                       TYPE: PRT
CORGANISM: Homo sapiens
US-10-094-886-172
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TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REPREEMENT: 2002-03-07
CURRENT APPLICATION NUMBER: 05/274,322
PRIOR PLING DATE: 2001-03-08
PRIOR PLING DATE: 2001-03-08
PRIOR PLING DATE: 2001-08-17
PRIOR PLING DATE: 2001-08-10
PRIOR PLING DATE: 2001-08-20
PRIOR PLING DATE: 2001-09-10
PRIOR PLING DATE: 2001-09-20
PRIOR PLING DATE: 2001-09-21
PRIOR PLING DATE: 2001-08-21
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PRIOR PLING DATE: 2001-08-21
PRIOR PLING DATE: 2001-08-21
PRIOR PLING DATE: 2001-08-21
  138 HIGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII 197
                                                                                         HLGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTBTRVRBII 180
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                                                                                                                                                                                                  QHPSAKGNLCPPTNETRKCTVQRKKCQKGERGTIIGEBKKK 238
                                                                                                                                                                           181 OHPSAKGNI, CPPTNETRKCTVQRKKCOKGBRGKKGRRRKRK 221
                                                                                                                                                                                                                                                                                                                          ; Sequence 172, Application US/10094886
; Publication No. US20040002120A1
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Padigaru, Muralidhara
Taupier, Raymond J., Jr.
Miller, Charles
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Liu, Xiaohong
Spytek, Kimberly A.
Patturajan, Meera
Burgess, Catherine
Vernet, Corine A.
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Pochart, Pascal
Fernandes, Elma
Shimkets, Richard
Rastelli, Luca
Spaderna, Steven
LaRochelle, William
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Boldog, Perenc
Guo, Xiaojia
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Zerhusen, Bryan
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Gangolli, Esha
Gusev, Vladimir
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                                                                                                                                                                                                                                                                                                                                            Publication No. US20
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 MECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQHPSAKGNLCPPTNETRKC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 CPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLHLGKCLDNCPEGLEANNHT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 MECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQHPSAKGNLCPPTNETRKC 199
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             PRIOR APPLICATION NUMBER: 60/274,281
PRIOR PELICATION NUMBER: 60/274,281
PRIOR PELICATION NUMBER: 60/274,281
PRIOR PLING DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-08-21
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-09
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PRIOR PLING DATE: 2001-06-07
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Badigaru, Muralidhara
Taupier, Raymond J., Jr.
Miller, Charles
Casman, Stacie
Penn, Carol
Gangolli, Esha
Gusev, Vladimir
Smithson, Glennda
Zerhusen, Bryan
Gerlach, Valerie
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Publication No. US20040002120A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
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Liu, Xiaohong
Spytek, Kimberly A.
Patturajan, Meera
Burgess, Catherine
Vernet, Corine A.
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Gorman, Linda
Malyankar, Uriel M.
Boldog, Ferenc
Guo, Xiaojia
FILING DATE: 2001-05-02
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### PREPLICANT: LANDING THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD FIRE REPRENCE: 21402-209.
#### PILE REPRENCE: 21402-209.
### PILE REPRENCE: 2001-03-08
## PILE REPRENCE: 2001-03-08
### PILE REPRENCE: 2001-03-09
### PILE R
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Job time : 37.6408 secs
Shimkets, Richard
Rastelli, Luca
Spaderna, Steven
LaRochelle, William
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Matches 192; Conservative
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ORGANISM: Homo sapiens
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OM protein - protein search, using sw model

June 29, 2004, 16:56:05; Search time 13.8641 Seconds (without alignments) 1887.186 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-894-912A-34 1510 1 MHLRLISMLFIILNPMBYIG......QQKKRKVQDKQKSVSVSTVH 272

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

SUMMARIES	Description	T43251 furin (BC 3.4.21.7	S34583 serine proteinase	JC5571 subtiliain-like pr	JC5570 subtilisin-like pr		A39490 subtilisin-like pr	B48225 probable proprotei		A48225 subtilisin-like pr	G02428 subtilisin-like pr	JC6148 subtilisin-like pr		A59180 Wht inhibitory fac	I53282 gene PACB4 protein	A47723 F-spondin precurso		A49175 Motch B protein -	A33837 insulin-like growt		A49128 cell-fate determin	T37314 probable kexin (BC	T27283 hypothetical prote	A38152 F-spondin - rat	B59180 Wnt inhibitory fac	C42125 trophozoite cystei	IGHUR1 insulin-like growt	A40043 notch protein homo	S70713 protein-tyrosine k	
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	ength I	1299	1548	962	975	1680	696	918	932	915	899	915	440	379	937	803	942	1203	1371	2524	2471	570	1620	603	378	677	1367	2555	1369	
di	Query Match Length DB	12.7	12.4	12.2	12.2	11.7	11.5	11.1	11.1	11.1	10.7	10.7	10.7	10.5	10.4	10.3	10.2	10.0	9.6	9.6	9.6	9.6	9.6	9.5	9.4	9.4	9.5	9.5	9.5	
	Score	192	186.5	184	184	176.5	173.5	168	167.5	167	162	162	161	158.5	156.5	156	153.5	150.5	149	148.5	147.5	145	145	143.5	142	142	139	139	138.5	
	Result No.	-	7	m	4	S	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	

S34583

Gerine proteinase (BC 3.4.21.-) PC6B - mouse
Grine proteinase (BC 3.4.21.-) PC6B - mouse
Grine proteinase (BC 3.4.21.-) PC6B - mouse
Grine for this musculus (house mouse)
Grine: 02-bec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
Grine: 02-bec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
Grine: 334583
Finakagawa, T.; Murakami, K.; Nakayama, K.
FEBS Lett. 327, 165-171, 1993
Finakagawa, T.; Murakami, K.; Nakayama, K.
FEBS Lett. 327, 165-171, 1993
Finakagawa, T.; Murakami, K.; Nakayama, K.
FEBS Lett. 327, 165-171, 1993
Finakagawa, T.; Murakami, K.; Nakayama, K.
FEBS Lett. 327, 165-171, 1993
Finakagawa, T.; Murakami, K.; Nakayama, K.
FEBS Lett. 327, 165-171, 1993
Finakagawa, T.; Murakami, K.; Nakayama, K.
FEBS Lett. 327, 165-171, 1993
Finakagawa, T.; Murakami, K.; Nakayama, K.
FEBS Lett. 327, 165-171, 1993
Finakagawa, T.; Murakami, K.; Nakayama, K.
FEBS Lett. 327, 165-171, 1993
Finakagawa, T.; Murakami, K.; Nakayama, K.
FEBS Lett. 327, 165-171, 1993
Finakagawa, T.; Murakami, K.; Nakayama, K.
FEBS Lett. 327, 165-171, 1993
Finakagawa, T.; Murakami, K.; Nakayama, K.
FEBS Lett. 327, 165-171, 1993
Finakagawa, T.; Murakami, K.; Nakayama, K.

RESULT 2

notch-1 protein -	transmembrane prot	insulin receptor-r	insulin receptor p	hypothetical prote	insulin receptor p	insulin receptor p	insulin receptor (	insulin receptor -	apoptosis-mediatin	insulin receptor-r	Notch homolog Moto	hypothetical prote	trophozoite surfac	furin (BC 3.4.21.7	cysteine rich prot
A46019	842612	B47417	INHUR	T26972	A34157	A36080	S57245	A56081	A46484	B36502	A48825	T22812	A48579	S43656	T42017
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2531	2437	540	1382	1111	1372	1383	2101	2148	327	1268	861	3871	667	837	1274
9.1 2531	9.1 2437	9.0 540	9.0 1382	_	_					8.5 1268					
9.1	137 9.1 2437	0.6	0.6	6.8	6.8	6.8		9.8	8.5		8.4	8.4	8.3		8.2

## ALIGNMENTS

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furin (EC 3.4.21.75) 2 - fruit fly (Drosophila melanogaster)
Cispecies: Drosophila melanogaster
Cispecies: Drosophila melanogaster
Cipate: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Mar-2000
CiAccession: A44344
R;Roebroek, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, E. A;Ticle: Chem. 267, 17208-17215, 1992
A;Title: Cloning and functional expression of Dfurinz, a subtilisin-like proprotein prox A;Reference number: A43434; WUID:92381036; PMID:1512259
767 CVTLCPAGFYADB -- SQKNCLKCHPSCKKCVDEPEKCTVCKEGFSLARGSCIPDCEPGTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Status: nucleic acid sequence not shown
                                                                                                                                                                               179 IIQHPSAKGNLC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-975 < MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Accession: JC5570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Gene: GDB: PACE4
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                                                                                                         a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R.Mori, K.; Kii, S.; Tsuji, A.; Nagahama, M.; Imamaki, A.; Hayashi, K.; Akamatsu, T.; Na Biochem. 121, 941-948, 1997
J. Biochem. 121, 941-948, 1997
J. Fitler. A novel human PACE4 isoform, PACE4E is an active processing protease containing A; Reference number: JCS570; MUID:97335942; PMID:9192737
A; Accession: JCS571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Cross-references: DDBJ:D87994; NID:g2330550; PIDN:BAA21792.1; PID:g2330551
A, Experimental source: brain cerebellum
C; Comment: This enzyme is a processing protease and responsible for processing of variou ch it is retained intracellularly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1
                              A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1548 «NAK>
A;Cross-references: GB:D17583; NID:9407344; PIDN:BAA04507.1; PID:d1005033; PID:g440374
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     splice form B-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  983 KTCEGNATSCNSCEGDFVLDHGVCWKTCPEKHVAVEGVCKHCPERCQDCIHEKTCKECMP 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---LECNGPKEDDCKVCADTS 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BVSEWNPWSPCTKKG-----KTC----GPKRGTETRVREIIQHPSAKGNL- 189
                                                                                                                                                                                                                                                                                                                                                           94 KCTKCKADCDTCFNKNPCTKCKS----GFYLALGKCLDNCPEGLEANNHTMB-CVSIVHC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 CLSSCPSGYYGTRYPDINKCTKCKADCDTCFNK-NFCTKCKSGFYLHLGKCLDNCPEGLE 134
                                                                                                                                                                                                                                                                                                                      38 SQGCQGGCATCSDYNG--CLSCKPRLFFALRRIGMRQIGVCLSSCPSGYYGTRYPDI--N 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subtilisin-like proprotein convertase (BC 3.4.21.-) PACB4 precursor, splice
C,Species: Homo sapiens (man)
Species: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C,Accession: JCS571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            925 SCEKCSEDCVSCSGADLCQQCLSQPDNTLLTHEGRCYHSCPEGFYAXDGVCEHCSS--PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----CPPT--NETRKCTVQRKKCQKGERGKKGRERKRKKPNKGESKEAIPDS
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                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Map position: 15q26-15q26
C;Superfamily: subtilisin-like proteinase PACB4; subtilisin homology
C;Superfamily: subtilisin-like proteinase
C;Keywords: glycoprotein; bydrolase; serine predicted <SIG>
F;1-62/Domain: signal sequence #status predicted <FRO>
F;196-434/Domain: propeptide #status predicted <FRO>
F;196-434/Domain: subtilisin homology <SBT>
F;938-954/Domain: hydrophobic cluster #status predicted <HCL>
F;205,246,347,420/Active site: Asp, His, Asm, Ser #status predicted
F;295/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .09
                                                                                                                                                                                                       DB 2; Length 1548;
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                                                                                                                                                                                                    Query Match 12.4%; Score 186.5; DB 2; Length 1
Best Local Similarity 25.0%; Pred. No. 6.9e-05;
Matches 66; Conservative 31; Mismatches 90; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .043 DFFLYNDMCHRSCPKSFYPDMRQCVPCHINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1092 KALHNGLCLDBCPEGTYKERENDE 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GDB:131390; OMIM:167405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 KSLESS---KEIPE----QRENKQ 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: nucleic acid sequence not shown
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   A; Accession: S34583
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C,Comment: This enzyme is a processing protease and responsible for processing of varion
ch it is retained intracellularly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: A novel human PACB4 isoform, PACB4B is an active processing protease containin: A;Reference number: JC5570; WUID:97335942; PMID:9192737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             splice form B-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                     subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form E C; Species: Homo sapiens (man)
C; Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C; Accession: JC5570
E; Managan: JC5570
J. Biochem: 121, S; Tsuji, A.; Nagahama, M.; Imamaki, A.; Hayashi, K.; Akamatsu, J. Biochem: 121, 941-948, 1997
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                                                                               875
-----VSIVHCEVS-EWNPWSPCTKKGKTCGFKRGTETRVRE 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GDB:131390; OMIM:167405
A;Map position: 15q26-15q26
C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C;Keywords: alternative splicing; glycoprotein; hydrolase; serine proteinase
F;1-62/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: DDBJ:D87993; NID:g2330548; PIDN:BAA21791.1; PID:g2330549
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                                                                               825 FDSELIRCGECHHTCGTCVGPGREECIHCAKNFHFHDW----KCVPACGEGFYPE----
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                                                                                                                                                                   ---PPTNBTRKCTVQRKKCQKGBRGKKGRBRKRKKPNKGE 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --EMPGLPHKVCRRYGPPGGE-ROATVS----SKGVPG--GOSLSASSPGAGE 932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.2%; Score 184; DB 2; Length 975; Best Local Similarity 26.6%; Pred. No. 7.2e-05; Matches 62; Conservative 24; Mismatches 87; Indels 6
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probable proprotein convertase (BC 3.4.21.-) 5 precursor - rat

N.Alternate names: PC5 precursor
C.Species: Rattus norvegicus (Norvay rat)
C.Species: Rattus norvegicus (Norvay rat)
C.Species: Rattus norvegicus (Norvay rat)
C.Species: B4825
R.Siusson, J.; Waau, D.; Hamelin, J.; Day, R.; Chretien, M.; Seidah, N.G.
R.Siusson, J.; Vaau, D.; Hamelin, J.; Day, R.; Chretien, M.; Seidah, N.G.
Proc. Natl. Acad. Sci. U.S.A. 90, 6691-6695, 1993
A.Title: cDNA structure of the mouse and rat subtilisin/kexin-like PCS: a candidate prop A;Reference number: A48225
A;Tatus: pellminary
A;Accession: B48225
A;Status: pellminary
A;Residues: pellminary
A;Residues: 1-915 < LUS>
A;Residues: 1-915 < LUS>
A;Cross-references: GB:L14933
C;Superfamily: subtilisin-like proteins predicted <SIG>C;Superfamil: signal sequence #status predicted <SIG>F;1-34/Domain: signal sequence #status predicted <SIG>F;1-34/Domain: signal sequence #status predicted <PRO>F;11-34/Domain: subtilisin homology <PROPPERSONERS F;10-915/Product: probable proproptein convertase 5 #status experimental <AMT>F;164-402/Domain: subtilisin homology <ASBT>F;173,214,388/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PACE4A - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
C;Accession: 155257
R;Hosaka, M.; Muzakami, K.; Nakayama, K.
Biomed. Res. 15, 383-339, 1994
A;Fille: PACE4A is a ubiquitous endoprotease that has similar but not identical substrate A;Reference number: 15527
A;Accession: 152227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 PDINKCTKCKADCDTCFNKNP--CTKCKSGFYLH--LGKCLDNCPBGLEANNHTMECVSI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 VHCEVSEWNPWSPCTKKGKTC-GPKRGTETRVREIIQHPSAKGNLCPPTNETRKCTVQRK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 YIGSQNASRGRRQRRMHPNVSQGCQGCATCSDYN--GCLSCKPRLFFALERIGMKQIGV 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 PNVSQ-GCQG----GCATCSDYNGCLSCKPRLFPALERIGMKQIGVCLSSCPSGYYGTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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A;Cross-references: GB:D50060; NID:g769700; PIDN:BAA08777.1; PID:g769701
C;Superfamily: subtilisin-like proteinase PACB4; subtilisin homology
F;172-410/Domain: subtilisin homology <SBT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.1%; Score 168; DB 2; 26.3%; Pred. No. 0.00076; tive 25; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.1%; Score 167.5; DB 2 24.1%; Pred. No. 0.00083; tive 25; Mismatches 78
                                       853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
                                   --TCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    740 -----GKCSENCKTCTGFHNCTE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52; Conservative
       838 FDSELIRCGECHH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 49; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 KCQKGE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form A - hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: A39490
R;Kiefer, M.C.; Tucker, J.E.; Joh, R.; Landsberg, K.B.; Saltman, D.; Barr, P.J.
DNA Cell Biol. 10, 757-769, 1991
A;Title: Identification of a second human subtilisin-like protease gene in the fes/fps
A;Reference number: A39490; MUID:92075167; PMID:1741956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1038 HLHVID-LAVCLQPCPDGYPENS----RNRTCVP-----CEPNCASCQDHPEYCTSCDHH 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------PCQEGCKTC----TSNGVCS 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCF--NKNPCTKCKSGF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 YLHLGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRV-R 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                737 YFGDTAARRCRR-----HHQEMNT 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 CLSSCPSGYYGTRYPDINKCTKCKADCDTCFNK-NFCTKCKSGFYLHLGKCLDNCPEGLE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CVTLCPAGPYADE -- SOKNCLKCHPSCKKCVDEPEKCTVCKEGPSLARGSCIPDCEPGTY 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 YIGSQNASRGRRQRRMHPNVSQGCQGCATCSD--YNGCLSCKPRLFFALBRIGMKQIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 HLRLISWLFIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDY-NGCLSCKPR
                                                            A;Molecule Cype: mRNA
A;Residues: 1.1680 <ROBS-
A;Cross-references: GB:M94375; NID:g157461; PID:g157462
A;Note: sequence extracted from NCBI backbone (NCBIN:111933, NCBIP:111934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gape
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A;Residues: 1-969 <KIE>
A;Cross-references: GB:M80482; NID:g189531; PIDN:AAA59998.1; PID:g189532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GDB:131390; OMIM:167405
A;Map position: 15q26-15q26
C;Superfamily: subtilisin-like proteinase PACB4; subtilisin homology
C;Superfamily: subtilisin-like proteinase PACB4; serine proteinase
C;Reyords: alternative splicing; hydrolase; serine proteinase
P;150-969/Product: serine proteinase PACB4 #status predicted <SIG>
P;196-434/Domain: subtilisin homology <SBT>
P;205,246,420/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.7%; Score 176.5; DB 2; Length 1680; 28.0%; Pred. No. 0.00033; vative 24; Mismatches 77; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.5%; Score 173.5; DB 1; Length 969; 28.8%; Pred. No. 0.00035; tive 16; Mismatches 54; Indels 39
                                                                                                                                                                                                                                                                      A,Cross-references: PlyBase:FBgn0004598
C;Superfamily: subtilisin homology
C;Keywords: hydrolase; serine proteinase; transmembrane protein
F;409-652/Domain: subtiliain homology <SBT>
F;418,457,638/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1178 BCLONWT-----LNKRDKCIVSGSEGCSESE 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 BIIOHPSAKGNLCPPTNETRKCTVQRKK-COKGE 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: kexin homolog
C;Species: Homo sapiens (man)
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Best Local Similarity 28.8*
Matches 44; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                       A;Status: preliminary
                                                                                                                                                                                                                                          A; Gene: PlyBase: Fur2
A; Accession: A43434
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Conservative
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A;Accession: G02428
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Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-915 <MIR>
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                                                                                                                   C; Accession: G02428
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                                                                                                                                                                                                                                                                                                                                                                                          Subtilisin-like proprotein convertase (EC 3.4.21.-) PC5 precursor - mouse NyAlternate names: kexin homolog; serine proteinase PC6 C;Species: Mus musculus (house mouse) (C;Species: Mus musculus (house mouse) (C;Date: 10.56p-1999 #sequence_revision 10.5ep-1999 #text_change 16-Jun-2000 (C;Accession: A48225; JX0248 (R;Lusson, J.; Vieau, D.; Hamelin, J.; Day, R.; Chretien, M.; Seidah, N.G. Proc. Natl. Acad. Sci. U.S.A. 90, 6691-6695, 1993 (A;Title: CDN attructure of the mouse and rat subtilisin/kexin-like PC5: a candidate prog A;Accession: A48225 (MUD:93342056; PMID:8341687) (A;Accession: A48225) (MUD:93342056; PMID:8341687)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-915 < LUS>
A; Rosadawa, T.; Hosaka, M.; Torii, S.; Watanabe, T.; Murakami, K.; Nakayama, K.
J. Blochem. 113, 132-135, 1993
A; Title: Identification and functional expression of a new member of the mammalian Kex2-A; Reference number: JX0248; MUID: 93224489; PMID: 9468318
A; Accession: JX0248
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A; Residues: 1-915 < NAS.
A; Residues: 1-915 < NAS.
A; Residues: 1-915 < NAS.
A; Cross-references: DDBJ: DD2619; NID:9220565; PIDN:BAA02143.1; PID:9220566
A; Rote: the authors translated the codon GGC for residue 915 as Ala
C; Superfamily: subtilisin-like proteinse PACE4; subtilisin homology
C; Superfamily: subtilisin-like proteinse PACE4; subtilisin homology
C; Keywords: duplication: glycoprotein; hydrolase; integrin binding; serine proteinase
F;1-34/Domain: signal sequence #status predicted < SIG>
F;1-16/Domain: propprotein provertase PC5 #status experimental < WAT>
F;117-915/Product: proprotein convertase PC5 #status experimental < WAT>
F;164-402/Domain: subtilisin homology < SET>
F;173,214,388/Active site: Asp, His, Ser #status predicted
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                                                CLSSCPSGYYGTRYPDINKCTKCKADCDTCPNK-NFCTKCKSGFYLHLGKCLDNCPEGLE 134
                                                                                                                                            ---VSIVHCBVS----EWNPWSPCTKKGKTCGFKRGTETR 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSCPSGYYGTRYPDINK--CTKCKADCDTCPNKNPCTKCKSGFYLHLGKCLDNCPEGLEA 135
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---HHQETNT 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 GSQNASRGRRQRRMHPNVSQGCQGCCATCSDYNG--CLSCKPRLFFALERIGMKQIGVCL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 KGKTC-----GPKR------GT---BTRVREIIQHPSAKGNLCPPTNETRKCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNSCLTCNGPGPKNCSSCPSGYLLDLGTCQMGAICKDATEESWAEGGFCMLVKKNNLC-
                                                                                                                                                                                          801 PDSBLVKCGECHHTCRTCVGPSREECIHCAKSFHPQDWKCVPACGE-----GF-----
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100 YPGDAARRCRR------CHKGCETCTGRSPAQCLSCR-RGPY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81; Indels
                                                                                                                                                                                                                                                                                            -----YPERMPGL--PHKVCRRCERNCLSCEGSSR 876
                                                                                                                                                                                                                                             176 VREIIQHPSAKGNLCPPTNBTRKCTVQRKKCQKGER 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 167; DB 1;
; Pred. No. 0.00089;
29; Mismatches 81;
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                                                                                                                                            135 ANNHTMEC-----
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Best Local Similarity
Matches 58; Conserva
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C;Species: Homo sapiens (man)
C;Species: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999
C;Accession: JC6148
C;Accession: JC6148
R;Miranda, L.; Wolf, J.; Pichuantes, S.; Duke, R.; Franzusoff, A.
Proc. Natl. Acad. Sci. U.S.A. 93, 7695-7700, 1996
A;Title: Isolation of the human PC6 gene encoding the putative host protease for HIV-1 of the A;Reference number: JC6148; MUID:96353880; PMID:8755538
A;Contents: CEM T-cell
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C,Comment: This protein functions as a soluble enzyme within the secretory pathway. It
- human (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 GKTC-----GFKRGTE-----TRVREIIQHPSAKGNLCPPTNBTRKCTV 201
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                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-899 <REU>
A;Cross-references: EMBL: U49114; NID:g1218057; PIDN:AAA91807.1; PID:g1218058
C;Genetics:
subtilisin-like proprotein convertase (BC 3.4.21.-) 5 precursor - human (fra
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 GSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNG--CLSCKPRLFFALERIGMKQIGVCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 SSCPSG-YYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLHLGKCLDNCPEGLEAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               663 GHYHADK-KRCRKCAPN-----CESCPGSHGDQCMSCKYGYPL-----NEBINSCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology C;Keywords: hydrolase; serine proteinase P;148-386/Domain: subtilisin homology <SBT>
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22.3%; Pred. No. 0.0019;
tive 33; Mismatches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.7%; Score 162; DB 2; 22.3%; Pred. No. 0.0019;
                                                                                                                      R;Reudelhuber, T.L.
submitted to the EMBL Data Library, February 1996
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C,Accession: 155282
R,Johnson, R.C.; Darlington, D.N.; Hand, T.A.; Bloomquist, B.T.; Mains, R.B.
R,Johnson, R.C.; Darlington, D.N.; Hand, T.A.; Bloomquist, B.T.; Mains, R.B.
R,Johnson, R.C.; Darlington, 1994
A,Title: PACR4: a subtlisin-like endoprotease prevalent in the anterior pituitary and A,Reference number: 153282; MUID:94349873; PMID:8070361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272 ------QCBISKCP--QPCRNGGKCIG---KSKCKCSKGYQGDLCSKPVCBPGCGAHG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 ČPGĠĊRNGGPĊNERRIĊECPDGFHGPHCEKALĊTPRCMWG------ĠLĊVTPGPCIĊ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 PSGYYGTRYPDINKCTKC-KADCD-TCFNKNPCTKCKSGFYLHLGKCLDNCPEGLEANNH 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 PPGFYG------VNCDKANCSTTCFNGGTC------FY--FGKCI--CPPGLEGE-- 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 TMBCVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTBTRVREIIQHPSAKGNLCPP----- 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193 -TNBTRKCTVQRKKCQKGERGKKGRRKKK-----KPNKGESKEAIPDSKSLESSKEIP 245
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A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-379 <HSI.
A;Cross-references: GB:AP122922; NID:g4585369; PIDN:AAD25402.1; PID:g4585370
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 CQGGCAT---CSDYNGC-----CLSCKPRLFFALERIGMKQIGVCLSS----C
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                                                                                                                                                                                                                                                     DB 2; Length 379;
                                                                                                                                                                                                                                           ch 10.5%; Score 158.5; DB 2; Similarity 24.9%; Pred. No. 0.0017; 60; Conservative 26; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 VREIIQHPSAKGNLCPPTNETRKCTVQRKKCQKGER 211
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-937 <RES>
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R;Hsleh, J.C.; Kodjabachian, L.; Rebbert, M.L.; Rattner, A.; Smallwood, P.M.; Samos, C.H.
Nature 398, 431-436, 1999
A;Title: A new secreted protein that binds to Wnt proteins and inhibits their activities
A;Reference number: A59180; WUID:99215557; PMID:10201374
A;Accession: A59180
                                                                                                                                                                                                                 | :| :| |: || GHYHADK-KRCAPN------CBSCFGSHGDQCMSCKYGYFL-----NBETNSCY 723
                                                                                                                                                         SSCPSG-YYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLHLGKCLDNCPEGLEAN 136
                                                                                                                                                                                                                                                                                                                                                           13.7 NHTMB-----NPWSPCTKK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 KPRLPFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNPCTKCKSG 117
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C;Species: Ceenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 21-Jan-2000
C;Accession: T24232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A59180
Wnt inhibitory factor-1 - human
C;Species: Homo sapiens (man)
C;Date: 18-Peb-2000 #sequence_revision 18-Peb-2000 #text_change 18-Peb-2000
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A;Introns: 36/3; 89/3; 179/2; 241/1; 306/1; 346/2
C;Superfamily: Caenorhabditis elegans hypothetical protein R17.3
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A;Molecule type: DNA
A;Residues: 1-440 <WIL>
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Best Local S
Matches 53
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61; Gaps

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F-spondin precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Bate: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Nov-2000
C;Accession: A47723
R;Ruiz i Altaba, A.; Cox, C.; Jessell, T.M.; Klar, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 8268-8272, 1993
A;Title: Ectopic neural expression of a floor plate marker in frog embryos injected with A;Title: Ectopic neural expression of a floor plate marker in frog embryos injected with A;Title: Ectopic neural expression of a floor plate marker in frog embryos injected with A;Accession: A47723
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10.3%; Score 156; DB 2; Length 803;
Best Local Similarity 24.6%; Pred. No. 0.0042;
Matches 58; Conservative 35; Mismatches 91; Indels
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Search completed: June 29, 2004, 17:03:06 Job time: 13.8641 secs

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The isoforms of proprocein convertase PC5 are sorted to different subcellular compartments.";
J. Cell Biol. 135:1261-1275(1996).

DEVELOPMENTAL EXPRESSION.
MEDLINE=9623359; PubMed=8698813;
Constam D.B., Calfon M., Robertson B.J.;
SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone morphogenetic proteins at distinct sites during embryogenesis.";
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Copyright (c) 1993 - 2004 Compugen Ltd.
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PCKS_BACC
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NTCZ_MOUSE
IGIR_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Comment=Additional isotorms seem to exist;
Name=PCCS; Symonyma=Long;
Name=PCSS; Symonyma=Long;
Isoid=Q04592-1; Sequence=Displayed;
Name=PCSS; Symonyma=Long;
Isoid=Q04592-2; Sequence=VSP 005438, VSP 005439;
Isoid=VSP SPCIPICITY: PCSA is expressed in most tissues but is most the intestine, adrenals and lung but not in the brain.
PVEX.OPENCENTAL STAGE: Weakly expressed throughout the embryo, except in the developing nervous system, the sibs and the liver, but markedly upregulated at discrete sites during development. At 86.5, abundant expression in differenciated decidua. At 87.5, intense expression in extraembryonic endoderm, and and hascells of limb buds). At 812.5, expression in the limbs is confined to the condensing mesenchym surrounding the cartilage. At this stage, strong expression also detected in vertebral and facial cartilage primordia and in the muscle of the tongue. At 816.5, abundant expression in epithelial cells of the intestinal villi. Isoform A is most abundant at all stages but significant levels of isoform B occur at 812.5.
IsoMAIN: The propeptide domain acts as an intramolecular chaperone assisting the folding of the zymogen within the endoplasmic refired.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                      of growth factors.

TATALYTIC ACTIVITY: Release of mature proteins from their proproteins by cleavage of Arg-Kaa-Yaa-ARG-|-Zaa bonds, where Kaa can be any amino acid and Yaa is Arg or Lys.

SUBCELLUIAL ROCATION: PC5A IS SECRETED THROUGH THE REGILATED SECRETORY PATHMAY. PC5B IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH
                                                                                                                                                                                                                                                                   for the maturation of gastrointestinal peptides. May be involved in the cellular proliferation of adrenal cortex via the activation of growth factors.
                                                                                                    Rancourt S.L., Rancourt D.B.,
"Murine subtilisin-like proteinase SPC6 is expressed during embryonic
"Murine subtilisin-like proteinase SPC6 is expressed during embryonic
implantation, somitogenesis, and skeletal formation.";
Dev. Genet. 21:75-81(1997).
-!- FUNCTION: Likely to represent a widespread endoprotease activity
within the constitutive and regulated secretory pathway. Capable
of cleavage at the RX(K/R)R consensus motif. May be responsible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN: AC 1 and AC 2 (clusters of acidic amino acids) contain sorting information. AC 1 directs TGN localization and interacts with the TGN sorting protein PACS-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to peptidase family S8. SIMILARITY: Contains 1 homo B/P domain.
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InterPro; IPR006212; Furin repeat.
InterPro; IPR009030; Grow_Eac_recep.
                                                                          MEDLINE=97436919; PubMed=9291583;
Cell Biol. 134:181-191(1996)
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                                                      DEVELOPMENTAL EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLY ENDOSOMES
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1209 NOPCHSSCKTC---NGSLCASCPTGMYLWLQ-----ACVPSCPGG----TWPSVTSG 1253
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ATEBSWAEGGPCMLVKKNNLCQRKVLQQLCCKTCTPQG
                                                                                                                                                                                                                                                                                     PROPROTEIN CONVERTASE SUBTILISIN/KEXIN
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Cleavage on pair of basic residues; Repeat; Alternative splicing;
Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                           AC 1.

AC 2.

CLEAVAGE (AUTO-) (BY SIMILARITY).

CELL ATTACHGENT SITE (POTENTIAL).

CHARGE RELAY SYSTEM (BY SIMILARITY

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MW; EC850E2DF20EA1C3 CRC64;
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                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL)
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InterPro; IPR002020; Protease Inhib.
Pfam; PF00082; Peptidase 58B.
PRIMTS; PR00082; Peptidase 58; 1.
PRIMTS; PR00723; SUBTILISIN.
ProDom; PD000717; P_domain; 1.
PROSTT; SM00261; FU; 22.
PROSITE; PS00136; SUBTILASE ASP; 1.
PROSITE; PS00138; SUBTILASE HIS; 1.
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InterPro, IPR000209; Peptidase_S8
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                             IsoId=09NJIS-3; Sequence=VSP 005442, VSP 005443;
-!- DOMAIN: The propeptide domain acts as an intramolecular chaperone assisting the folding of the zymogen within the endoplasmic
                                                                                          PCKS BRACL STANDARD; PRT; 1696 AA.

Q9NJ15; Q9NJ14; Q9NJ16;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 41, Last annotation update)
Proprotein convertase subtilisin/kexin type 5 precursor (RC 3.4.21.-)
(Proprotein convertase PC6-like) (APC6).
                                                                                                                                                                                                                       Branchiostoma californiensis (California lancelet) (Amphioxus).
Bukaryota, Metazoa, Chordata, Cephalochordata, Branchiostomidae,
                                                                                                                                                                                                                                                                                                   SEGUENCE FROM N.A. (ISOFORMS A; B AND C).
MEDLINE=20175281; PubMed=10708868;
Oliva A.A. Jr., Chan S.J., Steiner D.F.;
"Evolution of the prohormone convertases: identification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=09NJ15-2; Sequence=VSP_005444, VSP_005445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bvent=Alternative splicing; Named isoforms=3;

    -!- SIMILARITY: Belongs to peptidase family S8.
    -!- SIMILARITY: Contains 1 homo B/P domain.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q9NJ15-1; Sequence=Displayed;
InterPro; 1PR006212; Purin repeat.
InterPro; IPR009030; Grow fac_recep.
InterPro; IPR00209; Peptidase S8.
InterPro; IPR00284; Peptidase S8B.
InterPro; IPR0098020; Protease inhib.
Pfam: PF01483; P_proprotein; I.
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EMBL; AF184616; AAF26301.1; -.
EMBL; AF184617; AAF26302.1; -.
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MEROPS; S08.UPB; -.
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DDTCTACNDGFLLTDASSCEAGCP -> AENONQASPCPFA
PREVGVLAELALGHLRYSLTDVPPQSNSPPDTVLGADRARL
                                                                                                                                                                                                                                                                                                                                                                    CHPTCKECSDETDDTCTACNDGFLLTDASSCEAGCPPGQFL
HHGDCDSCHRECKTC -> IARCVDRRDRSWCDLVLRFNPC
VRRYFVKRCCGTCKLYMEDRPMRRGSSQPTQGRN (in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.2%; Score 184.5; DB 1; Length 1696;
22.7%; Pred. No. 6e-06;
tive 25; Mismatches 74; Indels 119; Gaps
                                                                      POTENTIAL. PROPROTEIN CONVERTASE SUBTILISIN/KEXIN
                                                                                                                                                                       CYS. RICH MOTIF (CRM) REGION.
CLRAVAGE (AUTO-) (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
Lydrolase, Serine protease, Glycoprotein; Zymogen; Signal; Clarvage on pair of basic residues; Repeat; Alternative splicing; SIGNAL
                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PURZ DROME STANDARD; PRT; 1679 AA.
P30412; 024301;
01-APR-1993 [Rel. 25, Created)
10-OCT-2003 [Rel. 41, Last sequence update)
10-OCT-2003 [Rel. 42, Last annotation update)
Purin-like protease 2 precursor [BC 3.4.21.75) [Furin 2).
PURZ OR CGIST3/4/CG4235.
BURSOSPHILS melanogaster (Fruit £1y).
BURANYOLA; Metaxoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1696 AA; 188410 MW; 281CBE1784257CBD CRC64;
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                                                                                                          EXTRACELLULAR (POTENTIAL)
                                                                                                                                CYTOPLASMIC (POTENTIAL).
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/FTId=VSP_005444.
Missing (in isoform A).
/FTId=VSP_005445.
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RX GENERAL MESERCELEY B. T. Folt R. A., Evans C. A., Gocayne J.D., R. Adams M.D., Celliker S. E., Holt R. A., Evans C. A., Galle R. F. Adams M.D., Celliker S. E., Mile P. W., Honkins R. A., Galle R. F. Amanatides P. G., Scheers S. E., Mis P. W., Honkins R. A., Galle R. F. Amanatides P. G., Scheers S. E., Mishads S. W. Redereson S. N., Sutton G. G. Mortman N. R. Yandell M. D., Zhang Q. Chen L. X., Bardon R. C., Rogers Y. H. C., Blasel R. G. Ester B. D., Raller C., Bardon B. P. Brandari D., Bolthakov S., Abhrill J. F., Agbayani A. Bardalale J. Bardakragoli U., Bealey B. R., Beenon K. Y., Benos P. W., Berman B. P. Brandari D., Bolthakov S., Burtis K. C., Busam D. A., Butler H., Cadisu E., Center A., Chandra I., Beenon K. J. W., Bernos P. W., Bernan B. P., Bhandari D., Bolthakov S., R. Burtis K. C., Busam D. A., Butler H., Cadisu E., Center A., Chandra I., Rutis R. Downes M. Dugarin-Boch S., Dunkov B. C., Dunn P., Burtis K. C., Busam D. A., Butler H., Cadisu E., Center A., Chandra I., R. Angeler C., Gabriellan A. E., Carris M. S., Dunkov B. C., Dunn P., Burtis K. D., Waller C., Cabrielar D., Houtin K. J., Evangeliata C. C., Ferraz C., Ferraz C., Ferrac S., Pleischmann W., Rallel F., Garg N. S., Gelbart W. M., Glasser K. Jalai M., Kaluuh F., Karpen G. H., Ke Z., Kennison J. A., Ketchum K. A., Jalai M., Kaluuh F., Karpen G. H., Ke Z., Kennison J. A., Ketchum K. A., Jalai M., Kaluuh F., Karpen G. H., Ke Z., Kennison J. A., Ketchum K. A., Jalai M., Kaluuh F., Mutris M. W., Mortmon W., Worlecod M. P., Backer D. L., Shellar Y. G. Mallai M., Kaluuh F., Sanders B., McInton M. V., Worlecod M. P., Backer D. L., Karpen G. B., Karpica G. D., Karaitz S., Kulp D., Lai Z., Mang X., Mutsu M., Mutris M., Mut
                                                                                                                       SEQUENCE FROM N.A.
STRAIN=Oregon-R, Tuebingen, and Iso-1;
STRAIN=Oregon-R, Tuebingen, and Iso-1;
MEDLINE=923810136; PubMed=1512259;
Rebbrock A.J.M., Creemers J.W.M., Pauli I.G.L., Kurzik-Dumke U.,
Rentrop M., Gateff E.A.P., Leunissen J.A.M., van de Ven W.J.M.;
"Cloning and functional expression of Diurin2, a subtilisin-like
proprotein processing enzyme of Drosophila melanogaster with multiple
repeats of a cysteline motif;",
J. Blol. Chem. 267:17208-17215(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=180-1;
MEDLINE=9518606, PubMed=7880443;
MEDLINE=9518606, PubMed=7880443;
Roebroek A.J.M., Ayoubi T.A.Y., Creemers J.W.M., Pauli I.G.L.,
van de Ven W.J.M.;
"The Dfurz gene of Drosophila melanogaster: genetic organization,
"The Dfurz gene of Drosophila melanogaster: genetic organization,
of its translational product Dfuring.";
DNA Cell Biol. 14:223-234(1995).
Ephydroidea, Drosophilidae, Drosophila
NCBI_TaxID=7227;
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SEQUENCE FROM N.A.
STRAIN=Berkeley;
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respective precursors. TISSUR SPECIFICITY: Transient expression in a subset of central

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nervous system neurons during embryonic stages 12-13. Expression in developing tracheal tree from stage 13 to end of embryonic
                                                                                                                                                                                                                                                                      R InterPro; IPRO06212; Furin repeat.
R InterPro; IPRO06212; Furin repeat.
InterPro; IPRO09030; Grow Fac recep.
InterPro; IPRO09030; Peptidase_S8.
R InterPro; IPRO09020; Protease_Inhlb.
R Ffam; Pro0062; Peptidase_S8.
R Pfam; Pro0062; Peptidase_S8; I.
R PFam; PRO0723; SUBTILISIN.
R ProDom; PO01717; P_domain; 1.
R SMART; SN00261; For interpression of the prosing subtiliable series and prosing subtiliable series.
R PROSITE; PS00137; SUBTILIASE_MSP; 1.
R PROSITE; PS00137; SUBTILIASE_MSP; 1.
R PROSITE; PS00138; SUBTILIASE_MSP; 1.
R Hydrolase; Series protease; Glycoprotein; Signal; Transmembrane;
                                   -1- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
10 X TANDEM REPEATS, CYS-RICH.
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N-LINKED (GLCNAC. .)
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N-LINKED (GLCNAC. .
MISSING (IN REF. 1)
V -> F (IN REF. 1).
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EMBL; AE003502; AAP48598.1;
PIR; A43434; A43434.
HSSP; Q99405; 1MPT.
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SIGNAL 1
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  1087 LVMHEHK------CYSACPLDTYET---EDNKCAPCHSTCATCNGPTDQDCITCRSSR 1135
                                                                                                                                                                                                                                                                                                        1136 YAWQNKCLISCPDGFYADKKRLECM------PCQEGCKTC----TSNGVCS 1176
                                                                                                                                      1037 HIHVID-LAVCLQPCPDGYPENS----RNRTCVP----CEPNCASCQDHPRYCTSCDHH 1086
                                               12;
                                                                                                                                                                                   118
                                                                                                                                                                                                                                                                            119 YLHLGKCLDNCPEGLEANNHTMECVSIVHCEVSEMNPWSPCTKKGKTCGFKRGTETRV-R 177
                                                                                             2 HLRLISWLFIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDY-NGCLSCKPR
                                                                                                                                                                                     LPPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCP--NKNFCTKCKSGP
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAC4 HUMAN STANDARD; PRT; 969 AA. P29122; O1099; O13100; O9UEG7; O9UEJ1; O9UEJ2; O9UEJ7; O9UEJ1; O9UEJ2; O9VEJ7; O9UEJ3; O9VEJ9; O9Y4G9; O9Y4H1; O1-DEC-1992 (Rel. 24, Created) O1-DEC-1992 (Rel. 24, Last sequence update) 15-MRA-2004 (Rel. 24, Last annotation update) 15-MRA-2004 (Rel. 34, Last annotation update) (Subtilisin/kexin-like protease PACE4) (Subtilisin/kexin-like protease PACE4) (Subtilisin-like proprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification of a second human subtilisin-like protease gene in the fess/fps region of chromosome 15."; DNA Cell Biol. 10:757-769(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identification of novel cDNAs encoding human kexin-like protease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mori K., Imamaki A., Kii S., Nagamune H., Nagahama M., Tsuji A.,
                                               53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUB=Placenta;
MEDLINE=94235049; PubMed=8179631;
Tsuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fauji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.
11.7%; Score 176.5; DB 1; Length 1679; 28.0%; Pred. No. 2.3e-05; ive 24; Mismatches 77; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS PACE4A-I AND PACE4B).
TISSUE-Hepatoma, and Kidney;
MEDLINE-92075167; PubMed=1741956;
Kiefer M.C., Tucker J.B., Joh R., Landsberg K.B., Saltman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matsuda Y.;
"Identification of a novel PACB4 isoform, PACB4B.";
Submitted (SBP-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. Biophys. Res. Commun. 204:1381-1382 (1994)
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                                                                                                                                                                                                                                                                                                                                                                      178 EIIQHPSAKGNLCPPTNETRKCTVQRKK-CQKGE 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95071480; PubMed=7980617;
                                                  60; Conservative
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  Query Match
Best Local Similarity
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Matsuda Y.;
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constitutive secretory pathway, with unique restricted
distribution in both neuroendocrine and non-neuroendocrine tissues
distribution in both neuroendocrine and non-neuroendocrine tissues
and capable of cleavage at the RK(R)R consensus motif.

-I- CATALYTIC ACTIVITY: Release of mature proteins from their
proproteins by cleavages of Arg-Kaa-RAG-|-Zaa bonds, where Xaa
can be any amino acid and Yaa is Arg or Lys.
-I- COPACTOR: Calcium (Potential).
-I- COPACTOR: Calcium (Potential).
-I- CUBMUNT: The PACEMA-I precursor protein seems to exist in the
reticulum endoplasmic as both a monomer, suggesting that
propeptide cleavage affects its tertiary or quaternary structure.
-I- SUBCELLUMAR LOCATION: PACEMA-I and PACEMA-II are secreted. PACEMC
and PACEMCS are not secreted and remain probably in zymogen form
in endoplasmic reticulum. PACEMB-I and PACEMB-II are retained
intracellularly probably through a hydrophobic cluster in their C-
terminus. PACEMB might be secreted.
                                  Mori K., Kii S., Tsuji A., Nagahama M., Imamaki A., Hayashi K., Akamatsu T., Nagamune H., Matsuda Y.; Andersu T., Nagamune H., Matsuda Y.; A novel human PACE4 isoforu, PACE4E is an active processing protease containing a hydrophobic cluster at the carboxy terminus."; J. Biochem. 121:941-948(1997).
                                                                                                                                                                                                                                                                                                                                                                                                          Tauji A., Hine C., Tamai Y., Yonemoto K., Mori K., Yoshida S.,
Bando M., Sakai E., Mori K., Akamatsu T., Matsuda Y.;
"Genomic organization and alternative splicing of human PACE4 (SPC4),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Bndoprotease PACE4 is Ca2+-dependent and temperature-sensitive and can partly rescue the phenotype of a furin-deficient cell strain."; siochem. J. 339:639-647(1999).
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                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS PACE4A-I; PACE4A-II; PACE4CS; PACE4D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=P29122-6; Sequence=VSP 005427, VSP_005434, VSP_005435;
Note=Probably enzymatically İnactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALTERNATIVE SPLICING (ISOPORM PACE4CS).
MEDLINE=97064242; PubMed=8906861;
Zhong M., Benjannet S., Lazure C., Munzer S., Seidah N.G.;
"Punctional analysis of human PACE4-A and PACE4-C isoforms:
identification of a new PACE4-CS isoform.";
PRBS Lett. 396:31-36(1996).
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Note=Probably enzymatically inactive;
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Name=PACB4A-1; Synonyms=PACB4;
IsoId=P29122-1; Sequence=Displayed;
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Isold=P29122-3; Sequence=VSP_005428,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kexin-like processing endoprotease.";
J. Biochem. 122:438-452(1997).
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                                                                                                                                                                                                                                                                                                                                     PACE48-I AND PACE4E-II).
MEDLINE=98021085; PubMed=9378725;
#EDLINE=97335942; PubMed=9192737;
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                    Name=PACE4E-II;
ISOIG=P29122-8; Sequence=VSP 005436, VSP 005437;
ISOIG=VSP SEGA in heart, brain, placenta, lung, skeletal muscle, kidney, pancreas, but at comparatively higher levels in the liver. PACE4A-II is at least expressed in placenta. PACE4B was only found in the embryonic kidney cell line from which it was isolated. PACE4C and PACE4D are expressed in placenta. PACE4E-I is expressed in cerebellum, placenta and pituitary. PACE4E-II is at least present in
                                                                                                                                      Cerebellum.

DOMAIN: The propeptide domain acts as an intramolecular chaperone sesisting the folding of the zymogen within the endoplasmic reticulum. Isoform PACE4D lacks the propeptide domain.
SIMILARITY: Belongs to peptidase family S8.
SIMILARITY: Contains 1 homo B/P domain.
SIMILARITY: Contains 1 pLAC domain.
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EMBL; M804812; AAA5998.1; -..

"WBL; AB00199; BAA21620.1; JOINED.

AB001900; BAA21620.1; JOINED.

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"21620.1; JOINED.
Name=PACE4E-1;
IsoId=P29122-7; Sequence=VSP_005437;
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76 CLSSCPSGYYGTRYPDINKCTKCKADCDTCPNK-NPCTKCKSGPYLHLGKCLDNCPRGLE 134
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                                                                                                                                                 18 YIGSONASRGRRQRRMIPNVSQGCQGGCATCSD--YNGCLSCKPRLPPALBRIGMKQIGV
                                                                                                                                                                                                                                                                                                                                                                                                PCKS_RAT STANDARD; PRT; 1877 AA.
P41413; Q62914;
01-NOV-1995 (Rel. 32, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Proprotein convertase subtilisin/kexin type 5 precursor (BC 3.4.21.-)
(Proprotein convertase PC5) (Subtilisin/kexin-like protease PC5)
(rPC5) (PC6) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20214819; PubMed=10749928; Xiang Y., Molloy S.S., Thomas L., Thomas G.; Xiang Y., Molloy S.S., Thomas L., Thomas G.; Thomas Fochs cytoplasmic domain contains two acidic clusters that direct sorting to distinct trans-Golgi network/endosomal compartments."; Mol. Biol. Cell 11:1257-1273 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97166043; PubMed=9013936;
Zheng M., Seidah N.G., Pinter J.B.;
"The developmental expression in the rat CNS and peripheral tissues
proteases PC5 and PACE4 mRNAs: comparison with other proprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Adrenal gland;
De Bie I., Marcinkiewicz M., Nakayama K., Lazure C., Seidah N.G.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Adrenal gland;
MEDLINE=93142056; PubMed=8341687;
MEDLINE=93420505; PubMed=8341687;
LUSSON J., Vieau D., Hamelin J., Day R., Chretien M., Seidah N.C
"CDNA structure of the mouse and rat subtilisin/kexin-like PC5:
candidate proprotein convertase expressed in endocrine and
nonendocrine cells.";
Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
                                                                                                                39;
                                                                               11.5%; Score 173.5; DB 1; Length 969; 28.8%; Pred. No. 2.2e-05; ive 16; Mismatches 54; Indels 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM SHORT), AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1676-1877 FROM N.A. (ISOFORM LONG).
                                                                                                                                                                                                                                                                                   135 ANNHIMBCVSIVHCEVSEWNPWSPCTKKGKTCG 167
                                                                                                                                                                                                                                                                                                                -----TCG 853
EMBL, AB001901; BAA21624.1; JOINED.
EMBL; AB001902; BAA21624.1; JOINED.
EMBL; AB001903; BAA21624.1; JOINED.
EMBL; AB001903; BAA21624.1; JOINED.
                                                                                                                                                                                                                                                                                                                  838 PDSELIRCGECHH------
                                                                                                                    44; Conservative
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                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                   Query Match
                                                                                                      Local
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Matches
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EVENTE-Alternative splicing; Named isoforms=2;

Comment=Additional isoforms seem to exist;

Name=PCSB; Synonyms=Short;
Isold=P41413-1; Sequence=Displayed;
Name=PCSA; Synonyms=Short;
Isold=P41413-2; Sequence=VSP 005440, VSP 005441;
Isold=P41413-1; Sequence=VSP 005440, VSP 005441;
Isold=P41413-1; Sequence=VSP 005441, 005441;
Isold=P414141-1*
Isold=P414-1*
Isol
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                can be any amino acid and Yaa is Arg or Lys.
SUBCELLULAR LOCATION: PCSA IS SECRETED THROUGH THE REGULATED
SUBCREICHY PATHWAY. PCSB IS A TYPE I NEWBRANE PROTEIN LOCALIZED TO
A PRARMUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH
RARLY ENDOSOMES (BY SIMILARITY).
proproteins by cleavage of Arg-Xaa-Yaa-ARG-|-Zaa bonds, where Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOWAIN. AC 1 and AC 2 (clusters of acidic amino acids) contain sorting information. AC 1 directs TGN localization and interacts with the TGN sorting protein PACS-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R InterPro; IPR006212; Purin repeat.
R InterPro; IPR00209; Peptidase_S8.
InterPro; IPR00209; Peptidase_S8.
R InterPro; IPR00209; Peptidase_S8.
R InterPro; IPR002010; Protecten; I.
R PRINTS; PR00723; SUBTILISIN.
R PRODOM; PD000717; P_domain; I.
R SWART; SW00261; FU; 6.
R PROSITE; PS00136; SUBTILASE_ASP; I.
R PROSITE; PS00138; SUBTILASE_ASP; I.
R PROSITE; PS00138; SUBTILASE_SER; I.
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BY SIMILARITY.
PROPROTEIN CONVERTASE SUBTILISIN/KEXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYS-RICH MOTIF (CRM) REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CATALYTIC.
HOMO B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SIMILARITY: Belongs to peptidase family SB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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EMBL; U47014; AAA87888.1; -.
PIR; B48225; B48225.
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SIGNAL
PROPEP 39
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90 PDINKCTKCRADCDTCPNKNP--CTKCKSGPYLH--LGKCLDNCPEGLEANNHTMECVSI 145
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092824; 013527;
16-0CT-2001 (Rel. 40, Last sequence update)
15-0KR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last snnotation update)
Proprotein convertase subtilisin/kexin type 5 precursor (BC 3.4.21.-)
Proprotein convertase PCS) (Subtilisin/kexin-like protesse PCS) (PC6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         683 ADKKRCRKCAPNCESCFGSHADQCLSCKYGYFLNEETSSCVAQCPEGSYQDIKKNIC---
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MEDLINE=56153880; PubMed=8755538;
Miranda L., Wolf J., Pichuantes S., Duke R., Franzusoff A.;
Miranda L., Wolf D., Pichuantes S., Duke R., Franzusoff A.;
HISolation of the human PC6 gene encoding the putative host protease for BIV-1 gpl60 processing in CD4+ T lymphocytes.";
Proc. Natl. Acad. Sci. U.S.A. 93:7695-7700(1996).
                                                                                                                                                                                                                                                                                                                                                                                                             CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Franzusoff A., Miranda L., Wolf J., Pichuantes S., Lu Y., Duke Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 11.1%; Score 168; DB 1; Length 1877; Local Similarity 26.3%; Pred. No. 0.0001; les 49; Conservative 25; Mismatches 54; Indels 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1877 AA; 207888 MW; 890955DC60534444 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Missing (In isoform PC5A). /FIId=VSP_005441.
                                                    CLEAVAGE (AUTO-) (BY CELL ATTACHMENT SITE
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SEQUENCE OF 15-913 FROM N.A.
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772 TCEDGQ 777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R SMART; SM0261; FU; 5.

R PROSITE; PS650900; PLAC; 1.

DR PROSITE; PS610136; SUBTILASE ASP; 1.

DR PROSITE; PS00137; SUBTILASE HIS; 1.

DR PROSITE; PS00138; SUBTILASE SER; 1.

DR PROSITE; PS00138; SUBTILASE SER; 1.

TW Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;

TM Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;

TM Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;

TM Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;

TM Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;

TM Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;

TM Hydrolase; Subtilasin/KEXIN

TM FROM Hydrolase; Subtilisin/KEXIN

TM FROM Hydrolase; Subtilisin/KEXIN

TM FROM Hydrolase; Subtilisin/KEXIN
Reudelhuber T.L.;
Submitted (FRB-1996) to the EWBL/GenBank/DDBJ databases.

-!- FUNCTION: Likely to represent a widespread endoprotesse activity
within the constitutive and regulated secretory pathway. Capable
of Cleavage at the RX(K/R)R consensus motif.

-!- CATALYTIC ACTIVITY: Release of mature proteins from their
proproteins by cleavage of Arg-Xaa-Yaa-ARG-|-Zaa bonds, where Xaa
can be any maino acid and Yaa is Arg or Lys.
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
                                                                                                                                                                                        IsoId=092824-1; Sequence=Displayed;
TISSUE SPECIFICITY: Expressed in T-lymphocytes.
DOWANT: The propeptide domain acts as an intramolecular chaperone
assisting the folding of the zymogen within the endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELL ATTACHMENT SITE (POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM, 600488; -. Gextracellular space; TAS. GG:0005515; F:serine-type endopeptidase activity; TAS. GG:0005615; F:serine-type endopeptidase activity; TAS. GG:0007267; P:cell-cell signaling; TAS. GG:0007267; P:cell-cell signaling; TAS. InterPro: IPR006121; Furin repeat. InterPro: IPR006212; Furin repeat. InterPro: IPR00212; Purin repeat. InterPro: IPR00213; Peptidase S8. InterPro: IPR002084; Peptidase S8. InterPro: IPR00183; Prorporotein; I. Pfam; PP01483; Pproprotein; I. Pfam; PP01083; Pproprotein; I. Pfam; PP000123; SUBTILISIN. PRODOM; PD000713; Pdomin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYS-RICH MOTIF (CRM) REGION.
                                                                                                                                             Event=Alternative splicing; Named isoforms=1;
Comment=2 isoforms may be produced;
                                                                                                                                                                                                                                                              SIMILARITY: Belongs to peptidase family S8 SIMILARITY: Contains 1 homo B/P domain. SIMILARITY: Contains 1 PLAC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U56387; AAC50643.2; --
EMBL; U39114; AAA91807.1; --
PIR; G02428; G02428
HSSP; Q99405; IMPT.
MEROPS; S08.076; --
Genew; HGNC:8747; PCSKS.
MIM; 600488; --
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78; Gaps 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 GKTC-----GPKRGTE-----TRVREIIQHPSAKGNLCPPTNETRKCTV 201
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Richards R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopking R.F., Jordan H., Moore T., Max S.II., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Carainar T. L., Scheetz T.B.,

Brownstein M.J., Usdin T.B., Tonahlow M.F., Carainar T.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A. Willalon D.K., Muray D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECURNCE FROM N.A.
MEDLINE=99215557; PubMed=10201374;
Heich J.-C., Kodjabachian L., Rebbert M.L., Rattner A.,
Smallwood P.M., Samos C.H., Nusse R., Dawid I.B., Nathans J.;
"A new secreted protein that binds to Wnt proteins and inhibits their activities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 SSCPSG-YYGTRYPDINKCTKCKADCDTCPNKNPCTKCKSGFYLHLGKCLDNCPBGLBAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                779 GODCOPCHRPCATCAGAGADGCINCTEGYFMEDGRCVQSCSISYYPDHSSENGYKSCKKC
                                                                                                                                                                                                                                                                                                                                                     20 GSONASRGRRORRMHPNVSQGCQGCATCSDYNG--CLSCKPRLFFALERIGMKQIGVCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
.) (POTENTIAL)
                                                                                                                                                                                                                                Match 10.7%; Score 162; DB 1; Length 913; Local Similarity 22.3%; Pred. No. 0.00014; Local Si, Conservative 33; Mismatches 81; Indels ...
802 N-LINKED (GLCNAC. . .) (POT
852 N-LINKED (GLCNAC. . .) (POT
121 V -> A (IN REF. 3) .
511 R -> A (IN REF. 3) .
601 R -> Q (IN REF. 3) .
101775 MW; 21389264CAD7546C CRC64;
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16-OCT-2001 (Rel. 40, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Wht inhibitory factor 1 precursor (WIF-1).
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813 AA;
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NCBI_TaxID=8355;
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WIF1 XENLA
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POTENTIAL.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR006209; BGF like.
InterPro; IPR006210; IBGF.
InterPro; IPR002010; IBGF.
InterPro; IPR002019; MIP.
InterPro; IPR002019; WIP.
InterPro; IPR002019; WIP.
InterPro; IPR00011; BGF.5.
InterPro; IPR0011; BGF.5.
IPR01115; PR00011; BGF.4.
IPR05112; PR00012; BGF.1; S.
IPR05112; PS00022; BGF.1; S.
IPR05113; PS50014; WIP; 1.
IPR05113; PS50014; WIP; 1.
IPR05114; PS50014; WIP; 1.
IPR05114; PS50014; WIP; 1.
IPR05115; PS50014; WIP; 1.
IPR05116; PS50014;
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Q -> L (IN REF. 1).
32EC54D60529EF96 CRC64;
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EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:18081; WIF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166
178
379 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P00743; 1CCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 605186
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16;

Gaps

83;

Conservative

Local Similarity es 60; Conserv

Best Loc Matches

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                           139 TMBCVSIVHCEVSEWNPWSPCTKKGKTCGPKRGTETRVREIIQHPSAKGNLCPP---- 192
                                                                                                                                                                                                                                         193 -TNETRKCTVORKKCOKGERGKKGRERKRK-----KPNKGESKEAIPDSKSLESSKEIP 245
                                                                                                                                                                                                                                                                  319 TCHEPNKC-----QCQEGWHGRHCKRYRASLIHALRPAGAQLRQHTPSLKKABERRDPP 373
                                                                               81 PSGYYGTRYPDINKCTKC-KADCD-TCFNKNPCTKCKSGFYLHLGKCLDNCPEGLEANNH 138
  80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 398:431-436 (1999).

-I- FUNCTION: Binds to WNT proteins and inhibits their activities. May be involved in mesoderm segmentation.
-I- SUBCELULIAR LOCATION: Secreted.
-I- TISSUB SPECIFICITY: During sometogenesis, expressed predominantly in unsegmented paraxial presomitic mesoderm and, to a much lesser extent, in newly segmented somites.
-I- DEVELOPMENTAL STAGE: First expressed at neurula stages.
-I- SIMILARITY: Contains 1 WIF domains.
                                                                                                      41 COGGCAT---CSDYNGC-----LSCKPRLFFALERIGMKQIGVCLSS----C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=99215557; PubMed=10201374;
HSieh J.-C., Kodjabachian L., Rebbert M.L., Rattner A.,
Smallwood P.M., Samos C.H., Nusse R., Dawid I.B., Nathans J.;
An new secreted protein that binds to Wnt proteins and inhibits their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
128-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
WNT inhibitory factor 1 precursor (WIP-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   374 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002049; Laminin EGF
InterPro; IPR003306; WIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AF122924; AAD25404.1; -. HSSP; P00740; 1BDM. INTERPRO; IPR006209; BGF like. InterPro; IPR006210; IBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PERM; PP00008; BGP; 5.
PERM; PP02019; WIP; 1.
PRINTS; PR00011; BGPLAMININ.
SWART; SW00181; EGF; 4.
SWART; SW00469; WIF; 1.
PROSITE; PS00022; BGF_1; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 YIGSQNASRGRRQRRMHPNVSQGCQGCCATCSDYN--GCLSCKPRLPPALERIGMKQIGV 75
                                                              pituitary and regulated by thyroid status.";
Endocrinology 135:1178-1185(1994).
-!- FUNCTION: Likely to represent an endoprotease activity within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWART; SMULAL, ..., PROSITE; PSSO900; PLAC; 1.
PROSITE; PSO130; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal; Calcium; Cleavage on pair of basic residues; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAIRED BASIC AMINO ACID CLEAVING ENZYME
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RELAY SYSTEM (BY SIMILARITY).
RELAY SYSTEM (BY SIMILARITY).
D (GLCNAC. .) (POTENTIAL).
D (GLCNAC. .) (POTENTIAL).
D (GLCNAC. .) (POTENTIAL).
"PACE4: a subtilisin-like endoprotease prevalent in the anterior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CELL ATTACHMENT SITE (POTENTIAL)
CHARGE RELAY SYSTEM (BY SIMILARI
CHARGE RELAY SYSTEM (BY SIMILARI
CHARGE RELAY SYSTEM (BY SIMILARI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104053 MW; P3865557C33705C8 CRC64;
                                                                                                                                                                                                                                                                      -1- SIMILARITY: Belongs to peptidase family S8.-1- SIMILARITY: Contains 1 homo B/P domain.-1- SIMILARITY: Contains 1 PLAC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.4%; Score 156.5; DB 1
23.6%; Pred. No. 0.00036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLEAVAGE (AUTO-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006212; Furin repeat.
InterPro; IPR000209; Peptidase SB.
InterPro; IPR002884; Peptidase SBB.
InterPro; IPR002080; Protease_Inhib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01483; P_proprotein; I.
Pfam; PF0082; Peptidase SB; 1.
PRINKS; PR0073; SUBTILISIN.
ProDom; PD000717; P domain; 1.
SMART; SM00261; FU; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, 131894; AAA61987.1; -. PIR; 153282.
HSSP, Q99405; 1MPT.
MEROPS; S08.075; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 51; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267 -----QCETSKCQ--QPCRNGGKCSG---KNKCKCSKGYQGDLCSKPVCBPSCGAHGTC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRANT'S-Spraque-Dawley; TISSUB-Hypothalamus, and Pituitary;
MEDLINE-94349873; PubMed-8070361;
Johnson R.C., Darlington D.N., Hand T.A., Bloomquist B.T., Mains R.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              228 PPGYYGINCDKVNCTTHC-LNGGTCP-----YPGKCI--CPSGYRGB----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CQGGCAT---CSDYNGC-----LSCKPRLFFALERIGMKQIGVC----LSSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 CTGGCRNGGFCNDRHVCECPDGPYGPHCBKALCMPRCMNG-----GLCVTPGLCIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSGYYGTRYPDINKCTKCKADCDTCPNKNPCTKCKSGFYLHLGKCLDNCPEGLEANNHTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 BCVSIVHCEVSEWNPWSPCTKKGKTCGPKRGTETRVRBIIQHPSAKGNLCPPTNBTRKCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    316 IBPUKCQCKE-GWNGRYCNKKYGSNIANALRPTGSRNRQHTPSPKRTEDRQALPB 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NVV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Paired basic amino acid cleaving enzyme 4 precursor (BC 3.4.21.-)
(Subtilisin/kexin-like protease PACB4) (Subtilisin-like proprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 VORKKCOKGERGKKGRERKRK------KPNKGESKEAIPDSKSLESSKEIPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.4%; Score 157.5; DB 1; Length 24.3%; Pred. No. 0.00013; ive 22; Mismatches 85; Indels
PROSITE; PS01186; EGF_2; 5.
PROSITE; PS50026; EGF_3; 4.
PROSITE; PS50814; WIF; 1.
Repeat; EGF-like domain; Signal; Developmental protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -LINKED (GLCNAC. . .) (PC
E26F973B0F00ACF8 CRC64;
                                                                                   POTENTIAL.
WNT INHIBITORY FACTOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        937 AA
                                                                                                                                EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5.
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POTENTIAL.
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01-NOV-1997 (Rel. 35, Last seq
15-MAR-2004 (Rel. 43, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41071 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 24.3 es 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                Wit signaling pathway.
SIGNAL 29
CHAIN 29 374
DOWAIN 172 203
DOWAIN 204 235
DOWAIN 268 267
                                                                                                                                                                                                        331.
181
187
195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       convertase 4) (SPC4).
PACE4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
                                                                                                                                                                                                                                                                                                                            DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41
                                                                                                                                                                                                                                                                                                                                                                                                                DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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ઠ 셤 ઠે 요 ઠે 셤 ò 셤 1

61; Gaps

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58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      brain.
                                                                           93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION.
                                                                                                                                                                                                                                                                                                                                                         NOTCH2
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 Matches
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                                                135 ANNHTMEC------VSIVHCEVS----EWNPWSPCTKKGKTCGFKRGTETR 175
                                                                           853
               CLSSCPSGYYGTRYPDINKCTKCKADCDTCPNK-NFCTKCKSGFYLHLGKCLDNCPEGLE 134
                                                                         806 FDSELIRCGECHHTCRTCVGPSREBCIHCAKSFHFQDWKCVPACGE-----GF-----
                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: Expressed at high levels in the floor plate.
-1- SIMILARITY: Contains 6 TSP type-1 domains.
                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F-SPONDIN.
TSP TYPE-1 1.
TSP TYPE-1 2.
TSP TYPE-1 3.
TSP TYPE-1 4.
TSP TYPE-1 5.
TSP TYPE-1 6.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -LINKED (GLCNAC. . .) (P. D3A54E329548AED9 CRC64;
                                                                                                  176 VREIIQHPSAKGNLCPPTNETRKCTVQRKKCQKGER 211
                                                                                                                           -----YPEEMPGL--PHKVCRRCDENCLSCEGSSR 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 156; DB 1;
Pred. No. 0.00034;
                                                                                                                                                                                                                01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FSB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                         803 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell adhesion
                                                                                                                                                                                                                                                                                                                                                          TISSUE=Embryo;
MEDLINE=93376785; PubMed=8367492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02014; Reeler; 1.
Pfam; PF00090; tsp_1; 6.
SWART; SW00209; TSP1; 6.
PROSITE; PS50092; TSP1; 6.
Glycoprotein; Signal; Repeat; Cd
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90702 MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A47723; A47723.
InterPro; IPR002861; Reeler.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L09123; AAA19105.1; -.
                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              489
                                                                                                                                                                                                                                                                                                   Xenopodinae; Xenopus.
NCBI TaxID=8355;
                                                                                                                                                                                                                                                    P-spondin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  803 AA;
                                                                                                                                                                                                                                                                                                                                           FROM N.A.
                                                                                                                                                                                        PSPO XENLA
                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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Length 803;

Query Match Best Local Similarity

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12;
                                                                                                                              544 VNEBCEPSSCIVIEWABWEBCS----ATCRMGMKKRHRMIKMTPADGSMCKADTIEVEK 598
                                                                                                                                                                               138 -HTMECVSIVHCEVSEMNPWSPCTKKCKTCGFKRGTETRVREIIQHPSAKGNLCPPTNET 196
                                   37 VSQCCQGGCATCSDYNGCLSCKPRLPPALERIGMKQIGVCLSSCPS--GYYGTRYPDINK
                                                                                                         C--TKCK------ADCDTCFNKNFCTKCKSGFYLHLGKCLDNCPBGLBANN---
                                                                                                                                                                                                                                                       197 RKCTVQRKKCQKGBRGKKGRERKRKKPNKGESKBAIPDSKSLESSKBIPEQRENKQ 252
                                                                                                                                                                                                                                                                          and adult
                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neurogenic locus notch homolog protein 2 precursor (Notch 2) (Motch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Mutation in ankyrin repeats of the mouse Notch2 gene induces early embryonic lethality.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRUGETHYMUS; STRUGETHE-CSPEL/6; TISSUE-THYMUS; ATAMAMADA Y., Higuchi M., Taujimoto Y.; "Complete amino acid sequence and mutliform transcripts encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRQUKNCB OF 1765-2153 FROM N.A.
MEDLINE-97075110; PubMed-8917536;
Milner L.A., Bigas A., Kopan R., Brashem-Stein C., Bernstein I.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 316-1518 FROM N.A.
SYATANE-CSTBL/6 X CRA; TISSUB-Embryo;
MEDLINE-93178563; PubMed-8440332;
Lardelli M., Lendahl U.;
"Motch A and Motch B-two mouse Notch homologues coexpressed in a wide variety of tissuses.";
Exp. Cell Res. 204:364-372(1993).
52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsujimoto Y.; in developing 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1699
MEDLINE-21523956; PubMed-11518718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Inhibition of granulocytic differentiation by mNotchl.";
Proc. Natl. Acad. Sci. U.S.A. 93:13014-13019(1996).
91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hamada Y., Kadokawa Y., Okabe M., Ikawa M., Coleman J.R.
Tsujimoto Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single copy of mouse Notch2 gene.";
Submitted (UUL-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Higuchi M., Kiyama H., Hayakawa T., Hamada Y., "Differential expression of Notch1 and Notch2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENTAL STAGE, AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brain Res. Mol. Brain Res. 29:263-272(1995).
 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  2470 AA
                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99396706; PubMed=10393120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95333893; PubMed=7609614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Development 126:3415-3424(1999).
                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                NTC2 MOUSE STANDARD 035516; 006008; 060941;
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POTENTIAL.

NUTCH EXTRACELLULAR TRUNCATION.

NUTCH EXTRACELLULAR TRUNCATION.

NUTCH EXTRACELLULAR DOMAIN.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CTTOPLASMIC (POTENTIAL).

EXP-LIKE 1.

EXP-LIKE 2.

EXP-LIKE 3.

EXP-LIKE 3.

EXP-LIKE 4.

EXP-LIKE 6.

EXP-LIKE 9.

EXP-LIKE 9.

EXP-LIKE 1.

EXP-LIKE 2.

EXP-LIKE 1.

EXP-LIKE 2.

EXP-LIKE 3.

CALCIUM-BINDING (POTENTIAL).

EXP-LIKE 2.

EXP-LIKE 2.

EXP-LIKE 3.

CALCIUM-BINDING (POTENTIAL).

EXP-LIKE 2.

EXP-LIKE 2.

EXP-LIKE 2.

EXP-LIKE 3.

CALCIUM-BINDING (POTENTIAL).

EXP-LIKE 2.

EXP-LIKE 2.

EXP-LIKE 2.

CALCIUM-BINDING (POTENTIAL).

EXP-LIKE 2.

EXP-LIKE 3.

CALCIUM-BINDING (POTENTIAL).

EXP-LIKE 3.

EXP-LIKE 3.

CALCIUM-BINDING (POTENTIAL).

EXP-LIKE 3.

CALCIUM-BINDING (POTENTIAL).

EXP-LIKE 3.

CALCIUM-BINDING (POTENTIAL).

EXP-LIKE 3.

EXP-LIKE 3.

CALCIUM-BINDING (POTENTIAL).

EXP-LIKE 3.

EXP-LIKE
         InterPro; IPR002110;
  not heart.

10 DBVBLOPMENTAL STAGE: Expressed in the embryonic ventricular zone, the postnatal ependymal cells, and the choroid plexus throughout embryonic and postnatal development.

11 ETM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a Cterminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presentlin dependent gamma-secretase to release a cleaved by presentlin dependent gamma-secretase to release a cleaved by presentlin dependent gamma-secretase to release a cleaved by presentlin dependent gamma-secretase to release a cleaved by presentlin dependent gamma-secretase to release a cleaved by the membrane.

10 Intractive contains 35 EGF-like domains.

21 SIMILARITY: Contains 21 Lin/Antch repeats.

22 IMILARITY: Contains 2 Lin/Antch repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RMBL outstation. The Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                 WEDLINE-21374376; PubMed-11459941;
WEDLINE-21374376; PubMed-11459941;
WAIZULANT. Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;
Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;
Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;
Toonservation of the biochemical mechanisms of signal transduction are among mammalian Norch family members.;
Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).
L. FUNCTION: Functions as a receptor for membrane-bound ligands Jaggedl and Deltai to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NAICD) it forms a transcriptional activator complex with RB-J kappa and activates genes of the enhancer of split locus.
C. Affects the implementation of differentiation, proliferation and appotence programs (By similarity). May play an essential role in specification and/or differentiation.
C. --- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-hands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=2;
Isold=035516-2; Sequence=VSP_001405;
Isold=O05estimental confirmation available;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Expressed in the brain, liver, kidney,
neuroepithelia, somites, optic vesicles and branchial arches, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D32210; BAA22094.1; -.
EMBL; X68279; CAA48340.1; -.
EMBL; W1881; AAC52924.1; -.
HSRP; D449175; A49175.
HSSP; D46109; 1458.
MGD; MGI:97364; Notch2.
GO; GO:0005887; C:integral to plasma membrane; IC.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:000211; P:morphogenesis of an epithelial sheet; IMP.
GO; GO:0007219; P:N signaling pathway; IC.
  Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.; "Murine notch homologs (NI-4) undergo presenilin-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bvent=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=1;
Isold=035516-1; Sequence=Displayed;
                        Droteolysis.";
J. Biol. Chem. 276:40268-40273(2001).
[7]
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bonds.

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                                                                                                                                                    Glycoprotein; ATP-binding; Phosphorylation; Repeat; Signal.
SIGNAL 1 30 POTENTIAL.
CHAIN 31 741 INSULIN-LIKE GROWTH PACTOR I RECEPTOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INSULIN-LIKE GROWTH FACTOR I RECEPTOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
 SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
PIBRONECTIN TYPE-III 1.
PIBRONECTIN TYPE-III 2.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC.
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  983 ENNIDECTE----SSCFNGGTCVDGINSPSCLCPVGFTGPFCLHDINECSSNPCLNAGT 1037
                                                              12;
                                                                                                   CLDN------CPEGLEANNHTMECVSIVH-CEVSEWNPWSPCTKKGKTCGPKRGTETRV 176
                                                                                                                                    90 P-DINKCTKCKADCDTCFNKNPC-------TRCKSGPYLHLGK 124
                                                                                    30 QRRMHPNVSQGCQGCCATCSDYNGCLSCKPRLPFALERIGMKQ1GVCLSSCPSGTYGTRY 89
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SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE PORMATION OF THE LIGAND-BINDING DOMAIN, WHILE THE BETA CHAIN CARRIES THE KINASE DOMAIN.
SUBCELLULAR LOCATION: Type I membrane protein.
SUBCLELULAR LOCATION: Type I membrane protein.
SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin receptor subfamily.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                           53; Indels 89; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Du J., Delafontaine P.;
"Inhibition of vascular smooth muscle cell growth through antisense transcription of a rat insulin-like growth factor I receptor cDNA."; circ. Res. 76:963-972(1955).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochém. Biophys. Res. Commun. 187:934-939(1992).
-!- FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IG
WITH A HIGH APPINITY AND IGF II WITH A LOWER APPINITY. IT HAS
TYROSINE-PROTEIN KINASE ACTIVITY.
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                                   10.0%; Score 150.5; DB 1; Length 2470; 24.3%; Pred. No. 0.0024; tive 23; Mismatches 53; Indels 89;
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Insulin-like growth factor I receptor precursor (BC 2.7.1.112)
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MEDLINE=22412145; PubMed=1530648;
Rurachi H., Jobo K., Ohta M., Kawasaki T., Itoh N.;
Fur achi H., albalin receptor family, insulin receptor-related receptor, is expressed preferentially in the
                                                                                                                                                                                                                                                   177 REIIQHPSAKGNLCPPTNETRKCTVQRKKC----QKG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor gene.";
Proc. Natl. Acad. Sci. U.S.A. 86:7451-7455(1989)
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MEDLINE=90017496; PubMed=2477843;
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           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Neurogenic locus notch protein homolog precursor (XOTCH protein)
                                                                                                                                                                                                                                  ch 9.9%; Score 149; DB 1; Length 1370; Similarity 26.7%; Pred. No. 0.0018; 47; Conservative 17; Mismatches 46; Indels 6
                                                                                                                                                                                1370 AA; 155395 MW; AS946897A41CB145 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=90385285; PubMed=2402639;
OGfman C., Harris W., Kintner C.;
"Xotch, the Xenopus homolog of Drosophila notch.";
Science 249:1438-1441(1990).
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InterPro; IPR00110; ANK.
InterPro; IPR00115; Ask hydroxyl_S.
InterPro; IPR00142; EGF_2.
InterPro; IPR001481; EGF_Ca.
InterPro; IPR001481; EGF_Ca.
InterPro; IPR001489; EGF_II.
InterPro; IPR002049; EGF_Iike.
InterPro; IPR002049; LamInin_EGF.
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REVISIONS TO 1759-1782.
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FUNCTION: Functions as a receptor for membrane-bound ligands Jagged1, Jagged2 and Deltal to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs. May play an essential role in postimplantation
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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MEDLINE-21331789; PubMed=11438922;
Irvin D.K., Zurcher S.D., Nguyen T., Weinmaster G., Kornblum H.I.;
"Expression patterns of Notchl, Notch2, and Notch3 suggest multiple functional roles for the Notch-DSL signaling system during brain development.";
J. Comp. Neurol. 436.167.107.
                                                                                                                        #; Score 148.5; DB 1; Length 2524;
#; Pred. No. 0.0035;
32; Mismatches 102; Indels 117;
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28-FEB-2003 (Rel. 41, Last annotation update)
Neurogenic locus notch homolog protein 2 precursor (Notch 2)
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MEDLINE=93202015; PubMed=1295745;
Weinmaster G.; Roberts V.J.; Lemke G.;
"Notch2: a second mammalian Notch gene.";
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28-FEB-2003 (Rel. 41, Created)
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nes 73; Conservative
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-!- DEWELOPWENTAL STAGE: Expressed in the brain during E14 and E17.
-!- PTM: Synthesized in the endoplasmic retlculum as an inactive form which is proteolytically cleaved by a furin-like convertace in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a Cterminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (WEXT). This fragment is then cleaved by presentlin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane [P8 similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its meeb by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
development, probably in some aspect of cell specification and/or differentiation (By similarity).

SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide bonds (By similarity).

SUBCELLULAR PLOCATION: Type I membrane protein. Following proteclytical processing NICD is translocated to the nucleus. TISSUE SPECIFICITY: Highly expressed in the spleen and choroid plexus in the brain. Expressed in postnatal central nervous system (CNS) germinal zones and, in early postnatal life, within numerous cells throughout the CNS. It is more highly localized to ventricular germinal zones. Also found in the heart, liver and
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NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN
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PROSITE; PS500297; ANK_REP_REGION; 1.

PROSITE; PS500297; ANK_REP_AT; 4.

PROSITE; PS00010; ASK_HTMROXYL; 22.

PROSITE; PS00186; EGF_1; 34.

PROSITE; PS50026; EGF_2; 26.

PROSITE; PS50026; EGF_2; 35.

PROSITE; PS10187; EGF_2; 26.

PROSITE; PS10187; EGF_2; 26.

PROSITE; PS10187; EGF_2; 26.

PROSITE; PS10187; EGF_2; 27.

PROSITE; PS10187; EGF_2; 27.

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PROSIDE; PS10187; EGF_2; 27.

PROSIDE; PS10187; 
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SIMILARITY: Belongs to the NOTCH family.
SIMILARITY: Contains 35 EGF-like domains.
SIMILARITY: Contains 2 Lin/Notch repeats.
SIMILARITY: Contains 6 ANK repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002110; ANK.
InterPro; IPR00152; Asx hydroxyl S.
InterPro; IPR000152; Asx hydroxyl S.
InterPro; IPR000181; EGF Z.
InterPro; IPR00181; EGF Z.
InterPro; IPR00181; EGF Z.
InterPro; IPR005209; EGF II.
InterPro; IPR005209; EGF II.ke.
InterPro; IPR005209; EGF II.ke.
InterPro; IPR005209; Notch.
InterPro; IPR00800; Notch.dom.
Pfam; Pf00001; ank; 6.
Pfam; Pf00001; EGF 35.
Pfam; Pf00001; EGF 35.
PROF; PRESPO279; Notch; 1.
PRINTS; PR00101; EGFEMON.
PRINTS; PR00101; EGFEMON.
PRINTS; PR0011; EGFEMON.
SWART; SM00148; ANK; 6.
SWART; SM00179; EGF ZA; 24.
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PIR; A49128; A49128.
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SIGNAL 1
CHAIN 26
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MEDLINE=20363723; PubMed=10903434;
985 ENNIDECTE----SSCFNGGTCVDGINSFSCLCPVGFTGPFCLHDINECSSNPCLNSGT 1039
                                                                                                                                                                                                                                  90 P-DINKCTKCKADCDTCFNKNFC-------TKCKSGFYLHLGK 124
                                                                                                                                                                                                                                                                 CLD-----NCPEGLEANNHTMECVSIVH-CEVSEWNPWSPCTKKGKTCGFKRGTETRV 176
                                                                                                                                                                                                                  OTDWINECLSEPCKING-GTCSDYVNSYTC-------TCPAGFHGVHC 984
                                                                                                                                                                                                   30 ORRMHPNVSQCCQGCCATCSDYNGCLSCKPRLPPALERIGMKQIGVCLSSCPSGYYGTRY 89
                                                                                                                                                                                     52; Indels 89; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                  | BL14 CAEEL | STANDARD; | PRT; | 943 AA. | P51559; O44762; O44763; O44764; O44765; O44766; O1-OCT-1996 (Rel. 34, Created) | C-1506 (Rel. 34, Created) | C-15003 (Rel. 41, Last sequence update) | 10-OCT-2003 (Rel. 42, Last annotation update) | Endoprotease bli-4 precursor (RC 3.4.21.-) (Blisterase) | Redoprotease bli-4 precursor (RC 3.4.21.-) (Blisterase) | Rel-4 OR KO4F10.4. | Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thacker C., Peters K.W., Srayko M., Rose A.W.;
"The bli-4 locus of Caenorhabditis elegans encodes structurally distinct kex2/subtilisin-like endoproteases essential for early development and the morphology.";
Genes Dev. 9:956-971(1995).
                                                                                                                                                                                                                                                                         ; Score 147.5; DB 1; Length 2471;
; Pred. No. 0.004;
23; Mismatches 52; Indels 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS A; B; C AND D), AND FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Bristol N2;
Latreille P., Wamsley P.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                            ---- QEKARPRCICPPGWDGAYCDVLNVSCKAAALQKG 1113
                                                                                                                                                                                                                                                                                              177 RELIQHPSAKGNICPPINETRKCTVQRKKC----QKG 209
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                      SIMILARITY.
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MEDLINE-95293228; PubMed=7774813;
9.88;
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                                                                                                                                                                                   54; Conservative
                                                                                                                                                                             Local Similarity
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MUTAGENESIS
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this tatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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R InterPro; IPR006212; Furin repeat.
R InterPro; IPR005030; Grow fac recep.
R InterPro; IPR002030; Grow fac recep.
R InterPro; IPR002030; Grow fac recep.
R InterPro; IPR002030; Poptidase_S8.
R InterPro; IPR003020; Poptidase_S8.
R Pfam; PF00483; Poptidase_S8; I.
R PRIMTS; RR00723; SUBTILISIN.
R PROMITS; RR00261; FU; J.
R RMART; SR00137; FU; J.
R PROSITE; PS00137; SUBTILASE_ASP; I.
R PROSITE; PS00137; SUBTILASE_RR; I.
R PROSITE; PS00138; SUBTILASE_RR; I.
R RR0128; Sering protease; Glycoprotein; Calcium-binding; Zymogen; SIGNAL 1 20 POTENTIAL.
Thacker C., Srayko M., Rose A.M.;
"Mutational analysis of bli-4/kpc-4 reveals critical residues required for proprotein convertase function in C. elegans.";
Gene 252.15-25(2000).
-!- FUNCTION: The Kex2/subtilisin-like proteinase activity of this enzyme is required for the normal production of adult cuticle.
There is functional redundancy between the isoforms. Vital for embryonic and larval development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note-No experimental confirmation available:
--- TISSUE SPECIFICITY: In larvae and adults, expressed in all hypodermal cells, vulva and ventral nerve cords.
--- DEVELOPMENTAL STAGE: Expression starts at embryo two-fold stage through to adults.
--- SIMILARITY: Belongs to peptidase family SB. Furin subfamily.
--- CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 651.
--- CAUTION: Ref.2 (AAB96754 and AAB96757) sequence differs from that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS; SOB.031; -...
WormPep; KO4F10.4a; CE11728.
WormPep; KO4F10.4c; CE11730.
WormPep; KO4F10.4c; CE11732.
WormPep; KO4F10.4c; CE11734.
WormPep; KO4F10.4c; CE11734.
GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0016021; F:setine-type endopeptidase activity; NAS.
GO; GO:0007592; P:cuticle biosynthesis (sensu Invertebrata); IMP.
                                                                                                                                                                                                                                                                                                                                                                                          Name=D; Synonyms=d;
IsoId=P51559-1; Sequence=Displayed;
Name=A; Synonyms=a;
IsoId=P51559-2; Sequence=VSP_005416, VSP_005419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=B; Synonyms=b;
IsoId=P51559-3; Sequence=VSP_005418, VSP_005421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=C; Synonyme=c;
IsoId=P51559-4; Sequence=VSP_005422, VSP_005423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSP 005420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                                                                                                                                          Event-Alternative splicing; Named isoforms=5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P51559-5; Sequence=VSP 005417,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF039719; AAB96753.1; ---
EMBL; AF039719; AAB96754.1; ALT_SEQ.
EMBL; AF039719; AAB96755.1; --
EMBL; AF039719; AAB96756.1; --
EMBL; AF039719; AAB96757.1; ALT_SEQ.
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EMBL; L29439; AAA98751.1; ALT_FRAME.
EMBL; L29440; AAA98752.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                ALTERNATIVE PRODUCTS:
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Search completed: June 29, 2004, 17:00:18 Job time: 9.25243 secs

Q91VK0 035171 Q8CFZ2 Q62030 Q86PQ3

Q96BP4 018003 Q9U018 042114

13222

035171 mus musculu Q86f22 mus musculu Q86p23 cryptospori Q96p4 homo sapien O18010 caenorhabdi O9018 giardia lam O42114 brachydanio O76822 branchiosto O462113 brachydanio O95v24 homo sapien Q96xx4 homo sapien Q96xy4 homo sapien Q9485 giardia lam Q80t14 mus musculu Q9w770 gallus gallus gallus Q9x70 gallus gallus Q9x70 gallus gallus Q9x70 gallus gallus Q9x62 homo sapien Q924y6 rattus norv Q94862 homo sapien Q92y6 homo sapien Q92y6 homo sapien Q93y70 gallus gallus gallus Q9x70 gallus gallus Q9x01 postori Q98c2 mus musculu Q8x28 mus musculu Q8x29 mus musculu Q9x29 mus musculu Q8x29 mus musculu Q9g41 giardia lam

042113 Q9PVZ4 O76510 Q86XX4 Q9GW45 Q9GQ45 Q80T14

Q924Y6 Q9HCB6 Q9HCB7 Q8NCD7 Q23832 Q9B105 Q9GLX9 Q99KR2

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1 MHLRLISWLFIILNFWEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR 60
                Thrombospondin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272;
172
167.5
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D9BXY4
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Q9ckB7 homo sapien
Q9csb2 mus musculu
Q8bvw2 mus musculu
Q9z132 mus musculu
Q9z135 homo sapien
Q8bfu0 mus musculu
Q8bfu0 mus musculu
Q7by3 homo sapien
Q7by3 mus musculu
Q8bj73 mus musculu
Q8bj73 mus musculu
Q8bj73 mus musculu
Q8bj74 entamoeba h
Q8szs2 drosophila
Q9sz442 entamoeba h
                                                 June 29, 2004, 16:55:24; Search time 34.6602 Seconds (without alignments) 2476.067 Million cell updates/sec
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                                                                                             1 MHLRLISWLFIILNFWEYIG......QQKKRKVQDKQKSVSVSTVH 272
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       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                             Potal number of hits satisfying chosen parameters:
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Gapop 10.0 , Gapext 0.5
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ALIGNMENTS

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Mao Y., Xie Y., Zhou Z., Zhao W., Zhao S., Wang W., Huang Y., Wang S.,
Tang R., Chen X., Wu C.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Buteleostomi;
Catarrhini; Hominidae; Homo.
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                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata;
Mammalla; Butheria; Primates;
NCBI_TaxID=9606;
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PRELIMINARY;
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Best Local Similarity
Matches 272; Conserva
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241 SKRIPBORENKOOOKKRKVODKOKS 265
                                                                                                                                                                          Mus musculus (Mouse).
                                                                                                                                                                                                                                       SEQUENCE PROM N.A.
                                                                                                                                                                                                            NCBI_TaxID=10090;
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SEQUENCE
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                                                             RESULT 3
Q9CSB2
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                                                                                                                                                    181 QHPSAKGWLCPPTWETRKCTVQRKKCQKGERGKKGRERKRKKPNKGESKEAIPDSKSLES 240
                                                     61 LFPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYL 120
                                                                                                    121 HLGKCLDNCPEGLEANNHTMECVSIVHCEVSEMNPWSPCTKKGKTCGFKRGTETRVREII 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LEPALERIGMKOLGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNPCTKCKSGFYL 120
                                                                                       121 HLGKCLDNCPEGLEANNHTWECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII 180
                                                                                                                                       QHPSAKGNLCPPTNBTRKCTVQRKKCQKGBRGKKGRBRKRKKPNKGBSKBAIPDSKSLBS 240
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                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Embryo;

A Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

A Nishikawa T., Nagai K., Sugiyama T., Otsuki T., Suzuki Y.,

A Nishikawa T., Nagai K., Sugaiya S., Kahashi-Tujii A., Hara H.,

A Arita M., Nahamura Y., Togiya S., Kawai Y., Saito K., Yamamoto J.,

A Arita M., Nakamura Y., Nagahari K., Masuho Y., Oshima A.,

"NEDO human CDNA sequencing project."; Masuho Y., Oshima A.,

"NEDO human CDNA sequencing project.";

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AK02746; BAB5501.1; -..

InterPro; IPR000030; Grow Fac_recep.

InterPro; IPR000030; Grow Fac_recep.

InterPro; IPR000030; TSP1.1.

RMART; SM00261; FU; 2.

SMART; SM00261; FU; 2.

RRART; SM00209; TSP1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                 Hypothetical protein FLJ14440.

Homo sapiens (Human).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Butheria, Primates; Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.5%; Score 1457; DB 4; Length 292; 99.2%; Pred. No. 2.7e-125; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 292 AA; 33243 MW; 01E2774AC3D4A6FB CRC64;
                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                       241 SKEIPEQRENKQQQKKRKVQDKQKSVSVSTVH 272
                                                                                                                                                                                                     241 SKEIPEQRENKQQQKKRKVQDKQKSVSVSTVH 272
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RC STRAING-57BL/63; TISSUB-Embryo; RX STRAING-57BL/63; TISSUB-Embryo; RX KWEN, N. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Shibata K., Yoshino H., Adachi J., Pukuda S., Arakawa T., Bara A., Pukunishi Y., Konoo S., Yamanaka I., Raito T., Okazaki Y., Gojobori T., Bono H., Kasukwa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T., Rakell P., Lewis S., Mateuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Ra Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Baronstein M.J., Bult C., Fletcher C., Pujita M., Gariboldi M., Rawaini M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Havachizaki V., Vanniki V., Kawai, H., Rohtsuki S.,
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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76.7%; Score 1158; DB 11; Length 217;
Best Local Similarity 93.1%; Pred. No. 4.5e-98;
Matches 202; Conservative 5; Mismatches 10; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9CSB2;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
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241 SKEIPEGRENKOOOKKRKVODKOKS 265
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THSD2 OR 2810459H04RIK.
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LERIGMKOIGVCLSSCPSGYYGTRYPDINKCTKCKAD-CDTCFNKNPCTKCKSGPYLHLG 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oshima A., Takahashi-Pujii A., Tanase T., Imose N., Takeuchi K., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Otsuki T., Satco H., Wakameteu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Mishikawa T., Kimura K., Yamashita H., Mateuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kamehori K., Sugiyama A., Kawakami B., Suzuki Y., Sugiyama A., Kawakami B., Suzuki Y., Nawuo buman cDNA sequencing project."; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                       Query Match 42.6%; Score 644; DB 11; Length 265;
Best Local Similarity 46.5%; Pred. No. 5.9e-51;
Matches 119; Conservative 36; Mismatches 77; Indels 24; Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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InterPro, IPR006212; Furin repeat.
InterPro, IPR009030; Grow_fac_recep.
InterPro; IPR00984; TSP1.
Pfam; PF00009; tsp. 1; 1.
SWART; SM00261; FU 2.
SWART; SM00209; TSP1; 1.
PR0SITE; PS0092; TSP1; 1.
SROATE; PS0092; TSP1; 1.
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Hypothetical protein.
SEQUENCE 236 AA; 25942 MW; 8D03803127EC5678 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ40906.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 AA
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Interpro; IPR009030; Grow Fac_recep.
Interpro; IPR00884; TSP1.
Pfam; PR00090; tsp_1; 1.
SMART; SM00261; FU; 2.
SMART; SM00261; TSP1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------RRHKGÖÖQ 247
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Matches 111; Conservative
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Best Local Similarity
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TISSUE-Uterus;
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QBN7L5
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X MEDLINE=22354683; PubMed=12466851;
X MEDLINE=22354683; PubMed=12466851;
A The FANTOM Consortium,
A the RIKEN Genome Exploration Research Group Phase I & II Team;
A the RIKEN Genome Exploration Research Group Phase I & II Team;
XT "Analysis of the mouse transcriptome based on functional annotation of R 60,770 full-length CDNAs.";
Nature 420:563-573 (2002)
BREL: AKO76308; BAC36296.1; -.
DR MGD: MGI:1920030; Thsd2.
DR MGD: MGI:1920030; Thsd2.
DR InterPro; IPR006212; Purin repeat.
DR SMART; SM00261; FU; 2.
SRQUENCE 224 AA; 25398 MW; BC13B083497CFRE3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LPFVLERIGAKQIGVCLSSCPSGYYGTRYPDINKCTKCKVDCDTCFNQNFCTKCKSGFYL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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"R-spondin, a novel thrombospondin type 1 domain gene, expressed in
the dorsal neural tube.";
Submitted (NuC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AB016768; BAA755601; -...
MGD; MGI:2183426; Rspondin.
                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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70.8%; Score 1069; DB 11; Length 224;
Best Local Similarity 84.7%; Pred. No. 6.5e-90;
Matches 188; Conservative 9; Mismatches 25; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 OHPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKK 222
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Thrombospondin type 1 domain.
                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                         224 AA.
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                                                                                                                                                                                                      Created)
                                                                                                                                      PRT;
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                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                             Thrombospondin homolog
THSD2 OR 2810459H04RIK
                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
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PRELIMINARY;
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  227 RAQB 230
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SEQUENCE
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Q8N6X6
                                                                         RESULT 8
                                                                                             Q9UGB2
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the the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
to 7.70 full-length cDNAs.";

Nature 420:563-573(2002)

R RMBL; AK049891; BAC33974.1; -.

R EMBL; AK049891; BAC33974.1; -.

R EMBL; AK049891; BAC33974.1; -.

R EMBL; AK049891; BAC39974.1; -.

R EMBL; AK049891; BAC39893.1; -.

R EMBL; AK040891; BAC39893.1; -.

R EMPC; IPR006621; Purin_repeat.

InterPro; IPR00684; TSP1.

R SMART; SM0020; TSP1.

R SMART; SM00209; TSP1: 1.

R PROSITE; PS50092; TSP1: 1.

W Hypothetical protein.

W Hypothetical protein.
                                                                                             92 INKCTKCKAD-CDTCFNKNFCTKCKSGFYLHLGKCLDNCPRGLEANNHTMBCVSIVHCEV 150
                                                                                                                      64 MNKCIKCKIEHCEACPSHNFCTKCKEGLYLHKGRCYPACPEGSSAANGTWECSSPACEV 123
                                                                                                                                                                                            151 SEWNPWSPCTKKGKTCGFKRGTETRVREIIQHPSAKGNLCPPTNETRKCTVQRKKCQKGE 210
                                                                                                                                                                                                                   119 LHRGRCFDECPDGFRAPLDETWECVE--GCEVGHWSEWGTCSRNNRTCGFRWGLETRIRGI 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LPPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKAD-CDTCFNKNFCTKCKSGFY 119
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                           RMHPNVSQGCQGCCATCSDYNGCLSCKPRLPPALERIGMKQIGVCLSSCPSGYYGTRYPD
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                          211 RGKKGRERKRKKPNKG----ESKBAIPDSKSLBSSKBIPBQRENKQQQKKR 257
                                                                                                                                                                                                                                                                                                                15;
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38.3%; Score 578.5; DB 11; Length 243;
Best Local Similarity 44.7%; Pred. No. 5.3e-45;
Matches 109; Conservative 39; Mismatches 81; Indels 15;
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01-MRR-2003 (TrEMBLrel. 23, Last sequence update)
10-CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical thrombospondin type I repeat.
2610028F08RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE-Eye, and Hippocampus; MEDLINE=22354683; PubMed=12466851; The PANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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SEQUENCE FROM N.A.
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QBBFU0;
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81 RGQEVNRCKKCGATCESCPSQDPCIRCKRQPYLYKGKCLPTCPPGTLAHQWTRBCQG--E 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 CEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQHPSAKGNLCPPTNETRKCTVQRKKCQ 207
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
01-MAY-2000 (TYEMBLrel. 13, Created)
01-CCT-2001 (TYEMBLrel. 18, Last sequence update)
01-CCT-2003 (TYEMBLrel. 25, Last annotation update)
DJ824F16.3 (Novel protein similar to mouse thrombospondin type 1
DJ824F16.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 31.3%; Score 472; DB 4; Length 22
Best Local Similarity 43.3%; Pred. No. 2.7e-35;
Matches 87; Conservative 36; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                Blakey S.; July 2001) to the EMBL/GenBank/DDBJ databases. Submitted (July 2001) to the EMBL/GenBank/DDBJ databases. EMBL, ALOS0325; CAB65783.3; -. Genew; HGNC:16175; C20orf182.
InterPro; IPR009512; Purin repeat.
InterPro; IPR009030; Grow_fac_recep.
InterPro; IPR009084; TSP1.
SMART; SM00261; PU; 2.
SWART; SM00261; TSP1; 1.
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: BC027938; AAH27938.1; -.
InterPro; IPR005212; Furin repeat.
InterPro; IPR009030; Grow_fac_recep.
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1 MRPCLPSFALIILNCMDYSQCQ-GNRWRRNKRA-SYVSNPICKGCLSCSKDNGCSRCQQK
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01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
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RX Strains-C57BL/6J; TISSUB-EBG9;

REDLINE-22388257; PubMed=12477932;

REDLINE-22388257; PubMed=12477932;

RAJURDE-C2388257; PubMed=12477932;

RAJURDE-C2388257; PubMed=12477932;

RA Altachal S.P., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,

RA Altachan B., Moore T., Max S.I., Wang J., Habte P.,

Didtchenko L., Warusina K., Parmer A.A., Rubin G.M., Hong L.,

Didtchenko L., Uordin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Stapleton M.J., Undin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Undin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Undin T.B., Roshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Hitchesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

RA Jones S.J., Marra M.A.,

RA Jones S.J., Marra M.A.,

RA Jones S.J., Marra M.A.,

RR Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences ",

Lyo. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                         118
                                                                                                                                                                                                                                                  70 MKQIGVCLSSCPSGYYGTRYPDINKCTKCKAD-CDTCFNKNPCTKCKSGPYLHLGKCLDN 128
                                                                                                                                                                                                                                                                                                                                                        129 CPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQHPSAKGN 188
                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                     1 MHLRLISWLPIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR
                                                                                                                                                                                                      Gaps
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                               30.4%; Score 459.5; DB 4; Length 176; 45.1%; Pred. No. 2.9e-34; Live 30; Mismatches 53; Indels 13.
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                                                                         PROSITE; PS50092; TSP1; 1.
SEQUENCE 176 AA; 20409 MW; 0FB3CCB1B2F8CAB5 CRC64;
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Last annotation update)
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STRAIN=C57BL/6J; TISSUE=Egg;
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nes 79; Conservative
InterPro, IPR000884; TSP1.
SMART; SM00261; FU; 1.
SMART; SM00209; TSP1; 1.
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Mus musculus (Mouse).
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01-0CT-2003
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59 LPFFLRREGWRQYGBCLHSCPSGYYGHRAPDMNRCARCRIENCDSCPSKDFCTKCKVGFY 118
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neopiera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae; Amphipyrinae; Spodoptera.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A930029K19RIK.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Ovary;
Cleplik W., Klenk H.;
"Cloning and functional characterization of FURIN from Spodoptera
frugiperda (Sf9) cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 RGOBANRCKKGGATCBSCFSQDFCIRCKRRFHLYKGKCLPSCPTG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 RYPDINKCTKCKADCDTCFNKNPCTKCKSGFYLHLGKCLDNCPEG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.8%; Score 283.5; DB 11; Length llarity 42.9%; Pred. No. 2.9e-18; Conservative 24; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00261; FU; 2. _ SEQUENCE 138 AA; 15172 MW; FBFD7D949279D5DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                               119 LHRGRCFDBCPDGFAPLDBTWBCVB--GCBVGHWS 151
                                                                                           120 LHLGKCLDNCPEGLEANNHTMECVSIVHCEVSEWN 154
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Protease.
SEQUENCE
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q964D2
Q964D2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
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GANGINOR F., Jegou S., Vallarino M., Vieau D., Vaudry H.;

GANGINOR F., Jegou S., Vallarino M., Vieau D., Vaudry H.;

"Wolecular characterization of the cDNA and localization of the mRNA encoding the prohormone convertase PC5-A in the European green frog.";

J. Comp. Neurol. 0:0-012002).

REMBL, AV131292; AAN10146-1; -.

GO; GO:0016020; G:membrane; IEA.

GO; GO:0016029; F:ATP binding; IEA.

GO; GO:0004313; F:Peptidase activity; IEA.

GO; GO:0004314; F:rensnembrane receptor protein tyrosine kin. ..; IEA.

R GO; GO:0006189; P:electron transport; IEA.

GO; GO:0006189; P:electron transport; IEA.

GO; GO:0006189; P:electron transport; IEA.

GO; GO:0006189; P:electron transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTKCKADCDTCP--NKNPCTKCKSGPYLHLGKCLDNCPEGLEANNHTMECVSIVHCEVSE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 WNPWSPCTKKGKTCGPKRGTETRVREIIQHPSAKGNLCPP---TNETRKC-TVQRKKCQK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---CSTCT-----SAPCLSCEPKWELNKKGKCMPVGSDKCSA 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 NVSQGCQGGCATCSD-YNGCLSCKPRLFFALERIGMKQIGVCLSSCPSGYYGTRYPDINK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serine protease PC5-A.
Rana esculenta (Edible frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
NCBI_TaxID=8401;
                                                                                                                                                  R GO; GO:000823); F:peptidase activity; IEA.

GO; GO:000823]; F:peptidase activity; IEA.

GO; GO:0004289; F:peptidase activity; IEA.

GO; GO:0004289; F:peptidase activity; IEA.

R InterPro; IPR00212; Furin repeat.

InterPro; IPR00212; Peptidase.SB.

InterPro; IPR00284; Peptidase.SB.

InterPro; IPR00384; Peptidase.SB.

InterPro; IPR00384; Peptidase.SB.

R InterPro; IPR00389; Peptidase.SB.

R Pfam; PR00483; P. proprotein; I.

R PRNTS; PR00723; SUBTILISIN.

R PRNAT; SW00241; FU; IO.

R PR0SITE; PS00134; SUBTILASE ASP; I.

R PROSITE; PS00134; SUBTILASE HIS; I.

R PROSITE; PS00138; SUBTILASE SIR; I.

R PROSITE; PS00138; SUBTILASE SIR; I.

R PROSITE; PS00138; SUBTILASE SIR; I.

R PROSITE; PS00138; SUBTILASE SIR; I.

R PROSITE; PS00138; SUBTILASE SIR; I.

R PROSITE; PS00138; SUBTILASE SIR; I.

R PROSITE; PS00138; SUBTILASE SIR; I.

R PROSITE; PS00138; SUBTILASE SIR; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 12.7%; Score 192; DB 5; Length 1299; Local Similarity 27.8%; Pred. No. 6.6e-09; es 63; Conservative 26; Mismatches 78; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209 GERGKKGRERKRKKPNK-----GESKE---AIPDSKSLESSKEIPE 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-1996) to the EWEL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
-!- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
EMBL; 748089; CAP43116.1; --
PIR; 743251; 743251.
HSSP; Q99405; IMPT.
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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97 KCKADCDTCF--NKNFCTKCKSGFYLH--LGKCLDNCPEGLBANNHTWECVSIVHCEVSE 152
                                                                       transmembrane receptor protein tyrosine kin. . .; IRA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 GGC-ATCSDYNGC----LSCKPRLFFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=HMN: IMSS;
MEDLINE=21391855; PubMed=11500468;
MEDLINE=21391855; PubMed=11500468;
Cheng X.J., Hughes M.A., Huston C.D., Loftus B., Gilchrist C.A.,
Lockhart L.A., Ghosh S., Miller-Sims V., Mann B.J., Petri M.A. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tachibana H.;
Intermediate Subunit of the Gal/GalNAc Lectin of Entamoeba
Intermediate Subunit of the Gal/GalNAc Lectin of Entamoeba
Intstolytica Is a Member of a Gene Family Containing Multiple CXXC
Sequence Motifs.;
Infect. Immun. 65:5892-5898(2001).
EMBL; AF313950; AAK92361.1; -..
GO, GO:0005529; F:sugar binding; IRA.
GO, GO:000157; P:heterophilic cell adhesion; IEA.
InterPro; IPR006209; EGF_like.
InterPro; IPR009309; GTow fac_recep.
PROSITE; PS01186; EGF_2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.9%; Score 179.5; DB 13; Length 913; 29.4%; Pred. No. 6.4e-08; ive 22; Mismatches 66; Indels 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               913 AA; 101864 MW; 6C9020632C47D9BB CRC64;
                    P:proteolysis and peptidolysis; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
GO; GO:0006508; P:proteolysis and pept GO; GO:0007169; P:transmembrane recept. InterPro; IPR006211; Purin-like.
InterPro; IPR006212; Purin repeat.
InterPro; IPR006212; Purin repeat.
InterPro; IPR006209; Portidase.
InterPro; IPR006209; Peptidase.
InterPro; IPR006209; Peptidase.
InterPro; IPR006209; Peptidase.
InterPro; IPR006209; Peptidase.
InterPro; IPR009209; Proprotein; I.Pfam; PF00483; Purin-like; I.Pfam; PF00483; Peptidase.
InterPro; IPR00181; EGF; 4.
IPR00FM; PR00181; EGF; 4.
IPR09FTS; PR00181; EGF; 4.
IPR09FTS; PR00130; SUBTILASE. ISP; I.PR005TTS; PR00173; SUBTILASE. ISP; I.PR05TTS; PR00173; SUBTILASE. ERR; I.PR05TTS; PR01785; I.PR05TTS; PR00178; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR05TTS; I.PR0
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Bukaryota; Entamoebidae; Entamoeba.
NCBL_TaxID=5759;
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119 YEHLGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRV-R 177
                                                                                                                                                                                                                                                         833 YANQNKCLISCPDGFYADKKRLECM------PCQEGCKTC----TSNGVCS 873
                              734 HLHVID-LAVCLQFCPDGYFENS----RNRTCVP----CEPNCASCQDHPEYCTSCDHH 783
                                                                                    61 LPPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCF--NKNFCTKCKSGP
                                                                                                                                                                                                                                                                                                                      178 BIIOHPSAKGNLCPPTNETRKCTVQRKK-CQKGE 210
                                                                                                                                                                                                                                                                                                                                                                               874 ECLONWI-----LINKRDKCIVSGSEGCSESE 899
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Job time : 35.6602 secs
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                                                                                          10;
                                                                                                                                                                                    89 YPDINKCTKCKADCDTCFNKOPCTK-----CKSGFYLHLGKCLDNCPEGLEA 135
                                                                                                                                                                                                                                                                                                                                                                                  136 NNHTMECVSIVHCEVSEWNPWSPCTKKG-KTC--GFKRGTETRVREIIQHPSAKGNLCPP 192
                                                                                                                                                                                                                                                                                                 S32 EGEKNGCAKCDDKCATCSDKDTCLTCADPLKVGSKCDGCKTGYYMSNGBC-----KPC 884
                                                                                                                                                                                                                                                                                                                                                                                                                                        ---YPDRIKGTCIPC 932
                                                                                                                                             43 GCCATCSD---YNGCL---SC----KPRLPPALE----RIGMKQIGVCLSSCPSGYYGTR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Prise B.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.B., Rubin G.M.,
                                                                                       80; Indela 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopterrygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                           11.7%; Score 177; DB 5; Length 1101; 26.6%; Pred. No. 1.3e-07; tive 22; Mismatches 80; Indels 5
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PROSITE; PS00136; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE ERR; 1.
HYGOLASE; Protease; Serine protease.
SEQUENCE 1376 AA; 149716 MW; B6704BAB9BABABFB CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Query Match
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